

AMENDMENT

In the Specification:

Please insert a new paragraph on page 1, beginning at line 4, immediately before the heading “BACKGROUND OF THE INVENTION”, as follows:

--SUBMISSION ON COMPACT DISC

The content of the following submission on compact discs is incorporated herein by reference in its entirety: A compact disc copy of the Sequence Listing (CRF) (file name: 514572002000, date recorded: June 9, 2006, size: 184,320 bytes); a duplicate compact disc copy of the Sequence Listing (COPY 1) (file name: 514572002000, date recorded: June 9, 2006, size: 184,320 bytes); and a duplicate compact disc copy of the Sequence Listing (COPY 2) (file name: 514572002000, date recorded: June 9, 2006, size: 184,320 bytes). --

Please replace Table 1, beginning on page 6, with a new Table 1 as follows:

Table 1. Exemplary Influenza A Virus Primers

Id	Sequence	SEQ ID NO:
PMIA_00001	TTTGTGCGACAATGCTTCA	<u>1</u>
PMIA_00002	GACATTGAGAAAGCTTGC	<u>2</u>
PMIA_00003	AGGGACAAACCTNGAACCTGG	<u>3</u>
PMIA_00004	AGGAGTTGAACCAAGACGCATT	<u>4</u>
PMIA_00005	ACCACATTCCCTTATACTGGAG	<u>5</u>
PMIA_00006	TTAGTCATCATCTTCTCACAAACA	<u>6</u>
PMIA_00007	ACAAATTGCTTCAAATGAGAAC	<u>7</u>
PMIA_00008	TGTCTCCGAAGAAATAAGATCC	<u>8</u>
PMIA_00009	GCGCAGAGACTTGAAGATGT	<u>9</u>
PMIA_00010	CCTTCCGTAGAAGGCCCT	<u>10</u>

Please replace Table 2, beginning on page 6 and bridging to page 7, with a new

Table 2 as follows:

Table 2. Exemplary Influenza B Virus Primers

<u>ID</u>	<u>Sequence</u>	<u>SEQ_ID NO:</u>
PMIB_00001	CACAATGGCAGAATTAGTGA	<u>11</u>
PMIB_00002	GTCAGTTGATCCCGTAGTG	<u>12</u>
PMIB_00003	CAGATCCCAGAGTGGACTCA	<u>13</u>
PMIB_00004	TGTATTACCCAAGGGTTGTTAC	<u>14</u>
PMIB_00005	GATCAGCATGACAGTAACAGGA	<u>15</u>
PMIB_00006	ATGTTCGGTAAAAGTCGTTTAT	<u>16</u>
PMIB_00007	CCACAGGGAGATTCCAAAG	<u>17</u>
PMIB_00008	GACATTCTTCCTGATTCTATAATC	<u>18</u>
PMIB_00009	CAAACAAACGGTAGACCAATATA	<u>19</u>
PMIB_00010	AGGTTCAAGTATCTATCACAGTCTT	<u>20</u>
PMIB_00011	ATGTCCAACATGGATATTGAC	<u>21</u>
PMIB_00012	GCTCTTCCTATAAATCGAATG	<u>22</u>
PMIB_00013	TGATCAAGTGATCGGAAGTAG	<u>23</u>
PMIB_00014	GATGGTCTGCTTAATTGGAA	<u>24</u>
PMIB_00015	ACAGAAAGATGGAGAAGGCAA	<u>25</u>
PMIB_00016	ATTGTTCTTGGCCTGGAT	<u>26</u>

Please replace Table 3, beginning on page 7, with a new Table 3 as follows:

Table 3. Exemplary Human Metapneumovirus Primers

<u>ID</u>	<u>Sequence</u>	<u>SEQ_ID NO:</u>
PMM_00001	CATCCCAAAATTGCCAGAT	<u>27</u>
PMM_00002	TTTGGGCTTGCCTTAAATG	<u>28</u>
PMM_00003	ACACCCCTCATCATTGCAACA	<u>29</u>
PMM_00004	GCCCTTCTGACTGTGGTCTC	<u>30</u>

<u>Id</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
PMM_00005	CGACACAGCAGCAGGAATTA	<u>31</u>
PMM_00006	TCAAAGCTGCTTGACACTGG	<u>32</u>
PMM_00007	CAAGTGCAGACATTGATGACC	<u>33</u>
PMM_00008	TAATTCCCTGCTGCTGTGTCG	<u>34</u>
PMM_00009	GCGACTGTAGCACTTGACGA	<u>35</u>
PMM_00010	TCATGATCAGTCCCGATAA	<u>36</u>
PMM_00011	TGTTTCAGGCCAATACACCA	<u>37</u>
PMM_00012	TCATGATCAGTCCCGATAA	<u>38</u>
PMM_00013	TCATGGGTAATGAAGCAGCA	<u>39</u>
PMM_00014	GGAGTTTTCCCATCACTGGA	<u>40</u>
PMM_00015	TCCAGTGATGGGAAACTCC	<u>41</u>
PMM_00016	TGTTGAGCTCCTTGCCTTT	<u>42</u>

Please replace Table 4, beginning on page 7 and bridging to page 9, with a new

Table 4 as follows:

Table 4. Exemplary Human Adenovirus Primers

<u>Id</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
PMAd1_00001	TGGCGGTATAAGGGTAACTG	<u>43</u>
PMAd1_00002	ATTGCGGTGATGGTTAAAGG	<u>44</u>
PMAd1_00003	TTTGCCGATCCACTTATC	<u>45</u>
PMAd1_00004	GCAAGTCTACCACGGCATT	<u>46</u>
PMAd2_00001	CTCCGTTATCGCTCCATGTT	<u>47</u>
PMAd2_00002	AAGGACTGGTCGTTGGTGTC	<u>48</u>
PMAd2_00003	AAATGCCGTGGTAGATTGC	<u>49</u>
PMAd2_00004	GTTGAAGGGGTTGACGTTGT	<u>50</u>
PMAd3_00001	TCCTCTGGATGGCATAGGAC	<u>51</u>

<u>Id</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
PMAd3_00002	TGTTGGTGTAGTGGGAAA	<u>52</u>
PMAd3_00003	ACATGGCCTGCAAAGTTCC	<u>53</u>
PMAd3_00004	GCATTGTGCCACGTTGTATC	<u>54</u>
PMAd4_00001	CGCTTCGGAGTACCTCAGTC	<u>55</u>
PMAd4_00002	CTGCATCATTGGTGTCAACC	<u>56</u>
PMAd4_00003	GGCACCTTTACCTCAACCA	<u>57</u>
PMAd4_00004	TCTGGACCAAGAACCAAGTCC	<u>58</u>
PMAd5_00001	GGCCTACCCCTGCTAACTTCC	<u>59</u>
PMAd5_00002	ATAAAGAAGGGTGGGCTCGT	<u>60</u>
PMAd5_00003	ATCGCAGTTGAATGCTGTTG	<u>61</u>
PMAd5_00004	GTTGAAGGGGTTGACGTTGT	<u>62</u>
PMAd7_00001	ACATGGCCTGCAAAGTTCC	<u>63</u>
PMAd7_00002	GATCGAACCTGATCCAAGA	<u>64</u>
PMAd7_00003	AACACCAACCGAAGGAGATG	<u>65</u>
PMAd7_00004	CCTATGCCATCCAGAGGAAA	<u>66</u>
PMAd11_00001	CAGATGCTGCCAACTACAA	<u>67</u>
PMAd11_00002	AGCCATGTAACCCACAAAGC	<u>68</u>
PMAd11_00003	ACGGACGTTATGTGCCTTTC	<u>69</u>
PMAd11_00004	GGGAATATTGGTTGCATTGG	<u>70</u>
PMAd21_00001	ACTGGTTCCCTGGTCCAGATG	<u>71</u>
PMAd21_00002	AGCCATGTAACCCACAAAGC	<u>72</u>
PMAd21_00003	CTGGATATGGCCAGCACTTT	<u>73</u>
PMAd21_00004	CACCTGAGGTTCTGGTTGGT	<u>74</u>

<u>Id</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
PMAd23_00001	TAATGAAAAGGGCGGACAAG	<u>75</u>
PMAd23_00002	GCCAATGTAGTTGGCCTGT	<u>76</u>
PMAd23_00003	AACTCCGCGGTAGACAGCTA	<u>77</u>
PMAd23_00004	CGTAGGTGTTGGTGTGGTG	<u>78</u>

Please replace Table 5, beginning on page 9, with a new Table 5 as follows:

Table 5. Exemplary HCoV-OC229E Primers

<u>Id</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
PMV_a0053	TCACTTGCTTCCGTTGAGGTTGGCTGGCGGTTAGAGTTGA	<u>79</u>
PMV_a0054	GGTTTCGGATGTTACAGCGTGTGCGACCGCCCTTGTATGG	<u>80</u>
PMV_a0055	TCACTTGCTTCCGTTGAGGCGTTGTTGGCCTTTCTTGTCT	<u>81</u>
PMV_a0056	GGTTTCGGATGTTACAGCGTGCCGGCATTATTCATTGTTCTG	<u>82</u>
PMV_a0057	TCACTTGCTTCCGTTGAGGACAAAAGCCGCTGGTGGTAAAG	<u>83</u>
PMV_a0058	GGTTTCGGATGTTACAGCGTCAGAAATCATAACGGGAAACTCA	<u>84</u>
PMV_a0059	TCACTTGCTTCCGTTGAGGAAGAGTTATTGCTGGCGTTGTGG	<u>85</u>
PMV_a0060	GGTTTCGGATGTTACAGCGTGCCGGCATTATTCATTGTTCTG	<u>86</u>
PMV_b0053	TTGGGCTGGCGGTTAGAGTTGA	<u>87</u>
PMV_b0054	GTGCGACCGCCCTTGTATGG	<u>88</u>
PMV_b0055	GCGTTGTTGGCCTTTCTTGTCT	<u>89</u>
PMV_b0056	GCCCGGCATTATTCATTGTTCTG	<u>90</u>
PMV_b0057	ACAAAAGCCGCTGGTGGTAAAG	<u>91</u>
PMV_b0058	CAGAAATCATAACGGGAAACTCA	<u>92</u>
PMV_b0059	AAGAGTTATTGCTGGCGTTGTGG	<u>93</u>
PMV_b0060	GCCCGGCATTATTCATTGTTCTG	<u>94</u>

Please replace Table 6, beginning on page 9 and bridging to page 10, with a new

Table 6 as follows:

Table 6. Exemplary HCoV-OC43 Primers

Id	Sequence	SEQ ID NO:
PMV_a0061	TCACTTGCTTCCGTTGAGGTTGGGTGATGGGTTTCAGATTAA	95
PMV_a0062	GGTTTCGGATGTTACAGCGTCTCGGAAAGATCGCCTTCTTCTA	96
PMV_b0061	TTGGGGTGTGGGTTTCAGATTAA	97
PMV_b0062	CTCGGGAAGATCGCCTTCTTCTA	98

Please replace Table 7, beginning on page 10 and bridging to page 11, with a new

Table 7 as follows:

Table 7. Exemplary Influenza A Virus Probes

Id	Sequence	SEQ ID NO:
PBIA_00001	TTTAGAGCCTATGTGGATGGATTCAAACCGAACGGCTGCATTGAGGGCAAGCTTCTCAAATGTC	99
PBIA_00002	ACAATTGAAGAAAAGATTGAAATCACTGGAACCATGCGCAGGCTTGCCGACCAAGTCTCCCACCGAAGT	100
PBIA_00003	AGCAATNGAGGAGTGCCTGATTAANGATCCCTGGGTTTGCTNAATGC	101
PBIA_00004	CCATACAGCCATGGAACAGGAACAGGATAACACCATGGACACAGTCAACAGAACACANCAATATTCAAGAAA	102
PBIA_00005	GGGCGGGGAGTCTCGAGCTCTCNGACGAAAAGGCAACGAACCCGATCGTGCC	103
PBIA_00006	GATCTNGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCTGACTAA	104

Please replace Table 8, beginning on page 11, with a new Table 8 as follows:

Table 8. Exemplary Influenza B Virus Probes

Id	Sequence	SEQ ID NO:
PBIB_00001	GCTGGGAAATAGCATGGAACGTGATGATATTCAAGCTACAATCAAGACTATTCTGTTAAGTAATGAATCCTCA	<u>105</u>
PBIB_00002	TCTGTTCCAGCTGGTTCTCCAATTTGAAGGAATGAGGAGCTACATAGACAAATAGATCCTAAAGGAG	<u>106</u>
PBIB_00003	TTACAACCATGAGCTACCAGAAGTTCCATATAATGCCTTCTTCTAATGTCTGATGAATTGGGCTGGCC	<u>107</u>
PBIB_00004	ACAAATAAGATCCAAATGAAATGGGAATGGAAGCTAGAAGATGTCTGCTTCAATCAATGCAACAAATGG	<u>108</u>
PBIB_00005	GAGGGAATGTATTCTGGAATAGANGAATGTATTAGTAACAACCCCTGGTAATACAGAGTGCATACTGGT	<u>109</u>
PBIB_00006	CTACCGTGTGGAGTAGCCGCACTAGGTATCAAAACATTGGAAACAAAGAAATCTTATGGATGGACT	<u>110</u>
PBIB_00007	GGCTATGACTGAAAAGATAACCAGAGACAGCCCAATTGGTCCGGGATTGGTATAGCACCAGTC	<u>111</u>
PBIB_00008	ACTGATCAGAGGAACATGATTCTGAGGAACAATGCTACGCTAAGTGTGCAAACCTTTGAGGCCTGTT	<u>112</u>
PBIB_00009	AAAATCCCTTGTNGGACATTGTCTATTGAGGGCATCAAAGANGCAGATATAACCCAGCACATGGTCC	<u>113</u>
PBIB_00010	CTTGGAAATACAAGGAATACAACCTAAAACAAATGCTGAAGACATAGGAACCAAGGCCAAATGTGCTCA	<u>114</u>
PBIB_00011	GTGGCAGGAGCAACATCAGCTGAGTTCATAGAAATGCTACACTGCTTACAAGGTGAAAATTGGAGACAA	<u>115</u>
PBIB_00012	GGAACCCATCCCCGAAAGAGCAACCACAAGCAGTGAAGCTGATGTCGGAAGGAAAACCCAAAAGAAACA	<u>116</u>
PBIB_00013	CTGTTCCAAAGATCAAAGGCCTAAACAGGCACAGAATTCAAGCCTAGATCAGCATTAAATCGTACCTTGAGGA	<u>117</u>
PBIB_00014	AGAGTTTGTCTGCATTAACAGGCACAGAATTCAAGCCTAGATCAGCATTAAATGCAAGGGTTCCATG	<u>118</u>
PBIB_00015	GAGGGACGTGATGCAGATGTCAAAGGAAATCTACTCAAGATGATGAATGACTCAATGGCTAAGAAAACCA	<u>119</u>
PBIB_00016	CCTATCAGGAATGGGAACACAGCAACAAAAAGAAAGGCCTGATTCTAGCTGAGAGAAAATGAGAAGA	<u>120</u>
PBIB_00017	GCAAGTCAAAAGAATGGGAAGGAATTGCAAAGGATGTAATGGAAGTGCTAAAGAGCTCTATGGGAA	<u>121</u>

Please replace Table 9, beginning on page 11 and bridging to page 12, with a new

Table 9 as follows:

Table 9. Exemplary Human Metapneumovirus Probes

Id	Sequence	SEQ ID NO:
PBM_00001	AAAAGTGTATCACAGAAGTTGTTCATTGAGTATGGCAAAGCATTAGGCTCATCATCTACAGGCAGCAAA	<u>122</u>
PBM_00002	GAAAGTCTATTGTTAATATATTATTCATGCAAGCTTATGGAGCCGGTAAACAAATGCTAAGGTGGGGGTCA	<u>123</u>
PBM_00003	ACGCTGTTGTTGGAGAAATTCTGTATGCTAACATGCTGATTACAAATATGCTGCAGAAATAGGAATAC	<u>124</u>
PBM_00004	TTAAGGAATCATCAGGTAATATCCCACAAAATCAGAGGCCCTCAGCACCAGACACACCCATAATCTTATT	<u>125</u>
PBM_00005	TGAGCAATCAAAGGAGTGCAACATCAACATATCCACTACAAATTACCCATGCAAAAGTCAGCACAGGAAGA	<u>126</u>
PBM_00006	CTGTTCCATTGGCAGCAACAGAGTAGGGATCATCAAGCAGCTGAACAAAGGTTGCTCCTATATAACCAAC	<u>127</u>
PBM_00007	ACTTAATGACAGATGCTGAACAGACTAGCCAGGGCGTTCTAACATGCCGACATCTGCAGGACAAATAAAATT	<u>128</u>
PBM_00008	AAAAAAAGGAAACTATGCTTGCCTCTTAAGAGAAGACCAAGGGTGGTATTGTCAGAATGCAGGTCAAC	<u>129</u>
PBM_00009	GAAAAGAACACACCAGTTACAATACCAGCATTATCAAATCGGTTCTATCAAAGAGAGTGAATCAGCCA	<u>130</u>
PBM_00010	CAAATCAGTTGGCAAAAAACACATGATCTGATCGCATTATGTGATTTATGGATCTAGAAAAGAACACA	<u>131</u>
PBM_00011	CAGCTAAAGACACTGACTATAACTACTCTGTATGCTGCATCACAAAGTGGCAATAACTAAAGTGAATG	<u>132</u>
PBM_00012	AAAAGAACACACCAGTTACAATACCAGCATTATCAAATCGGTTCTATCAAAGAGAGTGAATCAGCCAC	<u>133</u>
PBM_00013	CTATTATAGGAGAAAAAGTGAACACTGTATCTGAAACATTGGAATTACCTACTATCAGTAGACCCACCAA	<u>134</u>
PBM_00014	AAGTTAGCATGGACAGACAAAGGTGGGCAATCAAAACTGAAGCAAAGCAAACAAAGTATGGATGCTCTAGACTGCTTCAAGACAAT	<u>135</u>
PBM_00015	CAGGAAAATACACAAAGTTGGAGAAAGATGCTCTAGACTGCTTCAAGACAATGAAGAAGATGCAGA	<u>136</u>
PBM_00016	CTAATAGCAGACATAATAAGAAGCCAAGGGAAAAGCAGCAGAAATGATGGAAGAAGAAATGAACCGAC	<u>137</u>

Please replace Table 10, beginning on page 12 and bridging to page 13, with a new Table 10 as follows:

Table 10. Exemplary Human Adenovirus Probes

Id	Sequence	SEQ ID NO:
PBAd_00001	CTGACACCTACCAAGGTATAAAATCAAACGAAACGGTAATCCTCAAAACTGG ACCAAAATGACGATT	138
PBAd_00002	TCCCTACTCCAACATTGCACTGTACCTGCCTGACAAGCTAAAATACACTCCT ACAAATGTGAAATATC	139
PBAd_00003	GCTATCGGAGGCAGAGTACTAAAAAGACTACTCCCATGAAACCATGCTACGG ATCGTATGCCAGACCTA	140
PBAd_00004	AGTATTGTTTGTACAGTGAGGATGTTAATATGGAAACTCCTGATACTCACAT TTCATACAAACCAAGCA	141
PBAd_00005	GGGAAACGATCTTAGAGTTGACGGGGCTAGCATTAAGTTGACAGCATTGTC TTTACGCCACCTCTTC	142
PBAd_00006	TTGCCATTAACACCTCCTCCTGCCAGGCTCATATACATATGAATGGAAC TTCAGGAAGGATGTTAA	143
PBAd_00007	TTGCAACACGTAATGAAATAGGAGTGGGTAAACAACCTTGCCATGGAAATTAAAC CTAAATGCCAACCTATG	144
PBAd_00008	TTGGGGTAACTGACACCTATCAAGCTATTAAGGCTAATGGCAATGGCTCAGGC GATAATGGAGATATTAC	145
PBAd_00009	AGGTATCAAGGCATTAAGTTAAACCGATGACGCTAATGGATGGAAAAAGA TGCTAATGTTGATACAG	146
PBAd_00010	GAGAAGTTCTGTACTCCAATGTGGTTGTACCTCCAGATGTTACAAGT ACACGCCACCTAACATT	147
PBAd_00011	ATCAGTCATTAAACGACTACCTCTCTGCAGCTAACATGCTTACCCATTCT GCCAATGCAACCAACAT	148
PBAd_00012	CTACTTCGTATATTCTGGATCTATTCCCTACCTGGATGGCACCTTTACCTTA ACCAACACTTCAAGAAG	149
PBAd_00013	ACCTGCCAGTGGAGGATGCTAACAGCAAAATGCATACCTTGGGGTAGCTGC CATGCCAGGTGTTACTG	150
PBAd_00014	ATAGAAGCTGATGGCTGCCTATTAGAATAGATTCAACTTCTGGAAC TGACAC AGTAATTATGCTGATA	151
PBAd_00015	TTGAAATTAAGCGCACCGTGGACGGCGAGGGGTACAACGTGGCCAGTGCAAC ATGACCAAGGACTGGTT	152
PBAd_00016	CGGCAACGACCGGCTCCTGACGCCAACGAGTTGAAATTAGCGCACCGTGG ACGGCGAGGGTACAAC	153
PBAd_00017	CTCCAGTAACTTATGTCATGGCGCACTCACAGACCTGGCCAAAACCTTC	154

Id	Sequence	SEQ ID NO:
	TCTACGCCAACTCCGCC	
PBAd_00018	GCTAACCTCCCTATCCGTTATAGGCAAGACCGCAGTGACAGCATTACCA GAAAAAGTTCTTGCG	<u>155</u>
PBAd_00019	ACAGTCCTCCAACGTAAGGAAATTCTGATAACCCAAACACCTACGACTACATG AACAAAGCGAGTGGTGGC	<u>156</u>
PBAd_00020	AAGATGAACCTCCAAATTACTGCTTCCACTGGGAGGTGTGATTAATACAGAG ACTCTTACCAAGGTAAA	<u>157</u>
PBAd_00021	AGCTAACATGCTTACCCATCCCTGCCAATGCAACCAACATTCCAATTCCA TCCCATCTCGCAACTGG	<u>158</u>
PBAd_00022	TTCAACTCTGAAGCCATGCTGCGCAACGATACCAATGATCAGTCATTCAACG ACTACCTCTGCAGCT	<u>159</u>
PBAd_00023	AGGCTGTGGACAGCTATGATCCCGATGTTGTATTATTGAAAATCATGGCGTC GAGGATGAAGTGCCTAA	<u>160</u>
PBAd_00024	TGAAAATTGTGCTTACACGGAAAATGTCATTGGAAACTCCAGACAGCCATG TGGTATAACAAGCCAGGA	<u>161</u>
PBAd_00025	CATCGGCTATCAGGGCTTCTACATTCCAGAAGGATACAAAGATCGCATGTATT CATTTTCAGAAACTTC	<u>162</u>
PBAd_00026	GCTGCTTCTCCCAGGCTCCTACACTTATGAGTGGAACTTTAGGAAGGATGTGA ACATGGTTCTACAGAGT	<u>163</u>
PBAd_00027	ATGACACCAATGTCAGTCATTCAACGACTACCTATCTGCAGCTAACATGCTC TACCCCATTCCTGCCAA	<u>164</u>
PBAd_00028	CTTGCCAACATACAACATTGGATACCAGGGCTTACGTTCTGAGGTTACAA GGATCGCATGTACTCCT	<u>165</u>
PBAd_00029	GATCGCATGTACTCCTCTTCAGAAACTCCAGCCCAGTGGTAGACAGGTGGT TGATGAGATTAACATACA	<u>166</u>
PBAd_00030	CCCCTAACGGCGCTCCCAATACATCTCAGTGGATTGCTGAAGGCGTAAAAAAA GAAGATGGGGGATCTGA	<u>167</u>
PBAd_00031	AGAAAATGTAAATTGGAAACTCCAGATTCCATGTTGTTACAAAGCAGGAA CTTCAGACGAAAGCTCT	<u>168</u>
PBAd_00032	TGTGGCTACCAATACTGTTACCAAGGTGTAAAGTTACAAACTGGTCAAACGT ACAAATGGCAGAAAGAT	<u>169</u>
PBAd_00033	CCGAATTGGGAAGGGTAGCGTATTGCCATGGAAATCAATCTCCAGGCCAAC TGTGGAAAGAGTTCTG	<u>170</u>

Id	Sequence	SEQ ID NO:
PBAd_00034	TTGATGAGGTCAATTACAAAGACTTCAGGCCGTCGCCATACCCCTACCAACAC AACAACTCTGGCTTTGT	<u>171</u>
PBAd_00035	TGACGAAGAGGAAGAGAAAAATCTCACCACCTACACTTTGGAAATGCCAG TGAAAGCAGAAGGTGGT	<u>172</u>
PBAd_00036	AGAAGATTTGACATTGACATGGCTTCTTGATTCCAACACTATTAACACAC CAGATGTTGCTGTAT	<u>173</u>

Please replace Table 11, beginning on page 13 and bridging to page 14, with a new Table 11 as follows:

Table 11. Exemplary HCoV-OC229E Probes

Id	Sequence	SEQ ID NO:
PBS10049	AATGGGGTTATGTTGGTTCACTCTCCACTAATCACCATGCAATTGTAATGTTCA TAGAAATGAGCATGT	<u>174</u>
PBS10050	GTGTATGACTGCTTGTAAAGAATGTGGATTGGTCAATTACCTACCCATGATAG CTAATGAAAATGCCA	<u>175</u>
PBS10051	TTGCATCTCTTGTGGTATGCCATCTTGTGCATATGAAACAGCAAGACA AGAGTATGAAAATGC	<u>176</u>
PBS10052	AAATGGTTCCCTCACCAAAATAATCAAACAATTGAAGAAGGCTATGAATGTTGCA AAAGCTGAGTTGAC	<u>177</u>
PBS10053	CTGCTGCAGCTATGTACAAAGAACGACGTGCTGTTAATAGAAAATCAAAGTTGT TAGTGCATGCATAG	<u>178</u>
PBS10054	ACGTTGGACATGTCTAGTGTTGACACTATCCTTAATATGGCACGTAATGGTGT GTCCCTCTTCCGTT	<u>179</u>
PBS10055	CTGGTGGTAAAGTTCTTTCTGATGACGTTGAAGTAAAAGACATTGAACCTGT TTACAGAGTCAGCT	<u>180</u>
PBS10056	TTTACAGAGTCAGCTTGCTTGAGTTGAAGATGAAAAACTTGTAGATGTTG TGAAAAGCAATTGG	<u>181</u>
PBS10057	GATGTTGTGAAAAGGCAATTGGCAAGAAAATAAACATGAAGGTGACTGGGATA GCTTTGTAAAGACTA	<u>182</u>
PBS10058	GCGTTGTTGGCTTTCTGTCTAACGATAGTGATTTGGTCTGGTGATCTG TCGATTCTTATTGG	<u>183</u>

Id	Sequence	SEQ ID NO:
PBS10059	AGCAAGACAAGAGTATGAAAATGCTGTCGAAATGGTCCTCACCAAAATAATC AAACAATTGAAGAAG	<u>184</u>
PBS10060	TTGAAGAAGGCTATGAATGTTGCAAAAGCTGAGTTGACAGGAAATCATCTGTC AAAAGAAAATTAAACA	<u>185</u>
PBS10061	CTGCTGCAGCTATGTACAAAGAACGTGCTGTTAATAGAAAATCAAAAGTTGT TAGTGCCATGCATAG	<u>186</u>

Please replace Table 12, beginning on page 14, with a new Table 12 as follows:

Table 12. Exemplary HCoV-OC43 Probes

Id	Sequence	SEQ ID NO:
PBS10062	CTCACATCCTAGGAAGATGCATAGTTAGATGTTAAAGGTGAGAAGAATTGCATGACGATTAGTTA A	<u>187</u>
PBS10063	GGATTGGCCATTGCACCATAGCTCAACTCACGGATGCAGCAGTGTCCATTAGGAAAATGTTGATTAA T	<u>188</u>
PBS10064	GCATGCAATTCAATTATAAAATCACCATCAACCCCTCATCACCGGCTAGACTGAAATAGTTAACGCTCG G	<u>189</u>
PBS10065	ATAGTTAGTCACTGGATGGATTGTTGAATACACATCACCCACTGATAAGCTAGCTATGATTATG G	<u>190</u>

Please replace Table 13, beginning on page 23 and bridging to page 24, with a new Table 13 as follows:

Table 13. Exemplary SARS-CoV probes

probe_id	Sequence 5' - 3'	SEQ ID NO:	region
PBS00001	TTACCCCTAATATGTTATCACCCGCGAAGAAGCTATT CGTCACGTTCGTGCCTGGA	<u>191</u>	SARS-CoV Replicase 1B
PBS00002	CTGACAAGTATGTCGCAATCTACAACACAGGCTCTA TGAGTGTCTATAGAAAT	<u>192</u>	SARS-CoV Replicase 1B
PBS00003	CATAACACTTGCTGTAACCTATCACACCGTTCTACA GGTTAGCTAACGAGTGTGC	<u>193</u>	SARS-CoV Replicase 1B
PBS00004	TTACCCCTAATATGTTATCACCCGCGAAGAAGCTATT CGTCACGTTCGTGC	<u>194</u>	SARS-CoV Replicase 1B
PBS00009	GCGTTCTCTAAAGCTCCTGCCGTAGTGTCACTGATCA TCACCAAGATGCTGTTACTACATATAATGGATAC	<u>195</u>	SARS-CoV Replicase 1A

probe_id	Sequence 5'-3'	SEQ ID NO:	region
PBS00010	CTTTGGCTGGCTCTTACAGAGATTGGCCTATTCAAG ACAGCGTACAGAGTTAGGTGTTGAATTCTTAA	<u>196</u>	SARS-Cov Replicase 1A
PBS00011	CTACGTAGTGAAGCTTCGAGTACTACCATACTCTG ATGAGAGTTCTGGTAGGTACATGTCTGCTT	<u>197</u>	SARS-Cov Replicase 1A
PBS00012	TGCCAATTGGTTATGTGACACATGGTTTAATCTGA AGAGGCTGCGCGCTGTATCGCTCTCTAAAGC	<u>198</u>	SARS-Cov Replicase 1A
PBS00013	TATAAAAGTTACCAAGGGAAAGCCCGTAAAGGTGCTT GGAACATTGGACAACAGAGATCAGTTAACAC	<u>199</u>	SARS-Cov Replicase 1A
PBS00014	TGCTTCATTGATGTTGTTAACAAAGGCACTCGAAATGT GCATTGATCAAGTCACTATCGCTGGCGCAAAG	<u>200</u>	SARS-Cov Replicase 1A
PBS00015	TGTCGACGCCATGGTTATACTTCAGACCTGCTCACC AACAGTGTCAATTATGGCATATGTAAGTGGT	<u>201</u>	SARS-Cov Replicase 1A
PBS00016	TACTGTTGAAAAACTCAGGCCTATCTTGAATGGATT GAGGCAGAAACTTAGTGCAGGAGTTGAATTCTC	<u>202</u>	SARS-Cov Replicase 1A
PBS00017	ACCTATTCTGTTGCTTGACCAAGCTCTGTATCAGAC GTTGGAGATAGTACTGAAGTTCC	<u>203</u>	SARS-Cov Replicase 1A
PBS00018	GCCTATTAAATGTCATAGTTTGATGGCAAGTCCAAA TGCGACGGAGTCTGCTTCAAGTCTGCTTGTG	<u>204</u>	SARS-Cov Replicase 1A
PBS00019	TGAGAGCTAACACACTAAAGGTTCACTGCCTATTAA TGTCAAGTTTGATGGCAAGTCCAAATGCGA	<u>205</u>	SARS-Cov Replicase 1A
PBS00020	ACTTGCATGATGTGCTATAAGCGCAATCGTGCACAC GCGTTGAGTGTACAACATTGTTAATGGCATGA	<u>206</u>	SARS-Cov Replicase 1A
PBS00021	GGCGATGTTAGTGGCTATTGACTATAGACACTATTCA CGAGTTCAAGAAAGGTGCTAAATTACTGCATA	<u>207</u>	SARS-Cov Replicase 1A
PBS00022	TCAAACCAAACACTTGGTGTAACTGCTTGGAG TACAAAGCCAGTAGATACTCAAATTCAATTGA	<u>208</u>	SARS-Cov Replicase 1A
PBS00023	TAGTGCCTGGCAACATTGCTACACACCTTCCAAA CTCATTGAGTATAGTGAATTGCTAC	<u>209</u>	SARS-Cov Replicase 1A
PBS00024	TCATAGCTAACATCTTACTCCTCTTGTGCAACCTGT GGGTGCTTGTGCTGCTTCAGTAGTGGC	<u>210</u>	SARS-Cov Replicase 1A
PBS00025	GGTATTATTGCCATATTGGTGACTTGTGCTGCCACT ACTTTATGAAATTCAAGACGTGTTTGGTGAGT	<u>211</u>	SARS-Cov Replicase 1A
PBS00026	GTGATGTCAGAGAAACTATGACCCATCTTCTACAGCA TGCTAATTGGAAATCTGCAAAGCGAGTTCTTAA	<u>212</u>	SARS-Cov Replicase 1A
PBS00027	AACCATCAAGCCTGTGTCGATAAACACTCGATGGAGTT ACTTACACAGAGATTGAACCAAAATTGGATGGG	<u>213</u>	SARS-Cov Replicase 1A

probe_id	Sequence 5'-3'	SEQ ID NO:	region
PBS00028	GTTTTCTACAAGGAAACATCTTACACTACAACCATCA AGCCTGTCGTATAAACTCGATGGAGTTACTT	<u>214</u>	SARS-Cov Replicase 1A
PBS00029	CCTTGAATGAGGATCTCCTTGAGATACTGAGTCGTGA ACGTGTTAACATTAAACATTGTTGGCGATTTCA	<u>215</u>	SARS-Cov Replicase 1A
PBS00031	GCCATGGTTATACTTCAGACCTGCTCACCAACAGTG TCATTATTATGGCATATGTAACGGTGGTCTTG	<u>216</u>	SARS-Cov Replicase 1A
PBS00032	CAACAGACTTCTCAGTGGTTGCTAATCTTTGGCA CTACTGTTGAAAACCTAGGCCTATCTTGAAT	<u>217</u>	SARS-Cov Replicase 1A
PBS00033	TTCCCGTCAGGCAAAGTTGAAGGGTGCATGGTACAAG TAACCTGTGGAACCTACAAC	<u>218</u>	SARS-Cov Replicase 1A
PBS00034	GGTCACCACATCTGGTGTATCAGTGTGCCATGAGAC CTAATCATACCATTAAAGG	<u>219</u>	SARS-Cov Replicase 1A
PBS00035	AGATCATGTTGACATATTGGGACCTCTTCTGCTCAA ACAGGAATTGCCGTC	<u>220</u>	SARS-Cov Replicase 1A
PBS00036	TAAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAG CCTTGCGCAGAGACAAAAGAAGCAGCCCCT	<u>221</u>	SARS-Cov Nucleocapsid gene
PBS00037	ACGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACTT CTATTACCTAGGAACCTGGCCAGAGCTTC	<u>222</u>	SARS-Cov Nucleocapsid gene
PBS00038	GGCGCTAACAAAGAAGGCATCGTATGGGTTGCAACTG AGGGAGCCTTGAATACACCCAAAGACCACATTG	<u>223</u>	SARS-Cov Nucleocapsid gene
PBS00039	GTCCAGATGACCAAATTGGCTACTACCGAAGAGCTAC CCGACGAGTCGTGGTGGTACGGCAAAATGAA	<u>224</u>	SARS-Cov Nucleocapsid gene
PBS00040	GAGGTGGTGAAACTGCCCTCGCGCTATTGCTGCTAGA CAGATTGAACCAGCTTGAGAGCAAAGTTCTGG	<u>225</u>	SARS-Cov Nucleocapsid gene
PBS00041	AAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCCA GAGACAAAAGAAGCAGCCCCTGTGACTCTTCT	<u>226</u>	SARS-Cov Nucleocapsid gene
PBS00042	AAATTGCCACAATTGCTCCAAGTGCCTCTGCATTCTT TGGAATGTCACGCATTGGCATGGAAGTCACACC	<u>227</u>	SARS-Cov Nucleocapsid gene
PBS00043	ACCAATTAAACAAGGCATTAGTCACCAATTCAAGAAC ACTTACAAACAACATCAACTGCATTGGCAAGCT	<u>228</u>	SARS-Cov Spike glycoprotein gene
PBS00044	CACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCT ATATCAAGATGTTAACTGCACTGATGTTCTAC	<u>229</u>	SARS-Cov Spike glycoprotein gene
PBS00045	AAAGGGCTACCACCTTATGTCCTCCACAAGCAGCC CCGCATGGTGTGTTCTCCTACATGTCACGTAT	<u>230</u>	SARS-Cov Spike glycoprotein gene

probe_id	Sequence 5'-3'	SEQ ID NO:	region
PBS00046	TCAGGAAATTGTGATGTCGTTATTGGCATCATTAAACA ACACAGTTATGATCCTCTGCAACCTGAGCTTG	<u>231</u>	SARS-CoV Spike glycoprotein gene
PBS00047	TTGATCTTGGCGACATTCAGGCATTAACGCTTCTGT CGTCAACATTCAAAAAGAAATTGACGCCCTCAA	<u>232</u>	SARS-CoV Spike glycoprotein gene
PBS00048	GAGGAACCTCACCAACAGCGCCAGCAATTGTGATGAA GGCAAAGCATACTTCCCTCGTGAAGGTGTTTT	<u>233</u>	SARS-CoV Spike glycoprotein gene

Please replace Table 15, beginning on page 28 and bridging to page 38, with a new Table 15 as follows:

Table 15. Exemplary probes for non-SARS-CoV infectious organisms causing SARS-like symptoms

seqid	sequence(5'-3')	SEQ ID NO:	species
PBIA_00001	TTTAGAGCCTATGTGGATGGATTCTRAACCGAACGGC TGCATTGAGGGCAAGCTTCTCAAATGTC	<u>234</u>	Influenza A virus
PBIA_00002	ACAATTGAAGAAAAGATTGAAATCACTGGAACCATG CGCAGGCTTGCCGACCAAAAGTCTCCCACCGAACT	<u>235</u>	Influenza A virus
PBIA_00003	AGCAATNGAGGAGTGCTGATTAANGATCCCTGGGT TTTGCTNAATGC	<u>236</u>	Influenza A virus
PBIA_00004	CCATACAGCCATGGAACAGGAACAGGATAACCCATG GACACAGTCAACAGAACACANCAATATTCAAGAAA	<u>237</u>	Influenza A virus
PBIA_00005	GGCGGGGGAGTCTTCGAGCTCTCNGACGAAAAGGCA ACGAACCCGATCGTGCC	<u>238</u>	Influenza A virus
PBIA_00006	GATCTNGAGGCTCTCATGGAATGGCTAAAGACAAGA CCAATCCTGTCACCTCTGACTAA	<u>239</u>	Influenza A virus
PBIB_00001	GCTGGAAATAGCATGGAACTGATGATGATTTCAGCTA CAATCAAGACTATTGTTAAGTAATGAATCCTCA	<u>240</u>	Influenza B virus
PBIB_00002	TCTGTTCCAGCTGGTTCTCCAATTGAAAGGAATG AGGAGCTACATAGACAATATAGATCCTAAAGGAG	<u>241</u>	Influenza B virus
PBIB_00003	TTACAACCATGAGCTACCAGAACGTTCCATATAATGC CTTTCTCTAATGTCGATGAATTGGGCTGGCC	<u>242</u>	Influenza B virus
PBIB_00004	ACAAATAAGATCCAAATGAAATGGGAATGGAAGCT AGAAGATGTCGTTCAATCAATGCAACAAATGG	<u>243</u>	Influenza B virus
PBIB_00005	GAGGGAAATGTATTCTGGAATAGANGAACATGTATTAGT AACAAACCTTGGTAATACAGAGTGCATACTGGT	<u>244</u>	Influenza B virus
PBIB_00006	CTACCGTGTGGGAGTAGCCGCACTAGGTATCAAAA ACATTGGAAACAAAGAATACTTATGGATGGACT	<u>245</u>	Influenza B virus

seqid	sequence(5'-3')	SEQ ID NO:	species
PBIB_00007	GGCTATGACTGAAAGAATAACCAGAGACAGCCCAATTTGGTTCCGGGATTTTGTAGTATAGCACCGGTC	<u>246</u>	Influenza B virus
PBIB_00008	ACTGATCAGAGGAACATGATTCTGAGGAACAATGCTACGCTAAGTGTGCAACCTTTGAGGCCTGTT	<u>247</u>	Influenza B virus
PBIB_00009	AAAATCCCTTGACATTTGTCTATTGAGGGCATCAAAGANGCAGATATAACCCCAGCACATGGTCC	<u>248</u>	Influenza B virus
PBIB_00010	CTTGGAAATACAAGGGAAATACAACCTAAAACAAATGCTGAAGACATAGGAACCAAAGGCCAATGTGCTCA	<u>249</u>	Influenza B virus
PBIB_00011	GTGGCAGGAGCAACATCAGCTGAGTTCATAGAAATGCTACACTGCTTACAAGGTGAAAATTGGAGACAAA	<u>250</u>	Influenza B virus
PBIB_00012	GGAACCCATCCCCGGAAAGAGCAACCACAAGCAGTGAAAGCTGATGTCGGAAGGAAACCCAAAAGAAACA	<u>251</u>	Influenza B virus
PBIB_00013	CTGTTCCAAAGATCAAAGGCACCTAAAAGAGTTGGACTTGACCCTTCATTAATCAGTACCTTTGCAGGA	<u>252</u>	Influenza B virus
PBIB_00014	AGAGTTTGTCTGCATTAACAGGCACAGAAATTCAAGCCTAGATCAGCATTAAATGCAAGGGTTCCATG	<u>253</u>	Influenza B virus
PBIB_00015	GAGGGACGTGATGCGAGATGTCAAAGGAAATCTACTCAAGATGATGAATGACTCAATGGCTAAGAAAACCA	<u>254</u>	Influenza B virus
PBIB_00016	CCTATCAGGAATGGGAAACAACAGCAACAAAAAGAAAGGCCTGATTCTAGCTGAGAGAAAATGAGAAGA	<u>255</u>	Influenza B virus
PBIB_00017	GCAAGTCAAAAGAATGGGAAGGAATTGCAAAGGATGTAATGGAAGTGCTAAAGCAGAGCTCTATGGAA	<u>256</u>	Influenza B virus
PBAd_00001	CTGACACCTACCAAGGTATAAAATCAAACGGAAACGCTAAATGACGATT	<u>257</u>	Human adenovirus
PBAd_00002	TCCTCTACTCCAACATTGCACTGTACCTGCCTGACAAGCTAAATACACTCCTACAAATGTGGAAATATC	<u>258</u>	Human adenovirus
PBAd_00003	GCTATCGGAGGCAGAGTACTAAAAAGACTACTCCCCTGAAACCATGCTACGGATCGTATGCCAGACCTA	<u>259</u>	Human adenovirus
PBAd_00004	AGTATTGTTTGACAGTGAGGATGTTAATATGGAAACTCCTGATACTCACATTCTACAAACCAAGCA	<u>260</u>	Human adenovirus
PBAd_00005	GGGAAACGATCTTAGAGTTGACGGGGCTAGCATTAACTTGTACGCCACCTCTTC	<u>261</u>	Human adenovirus
PBAd_00006	TTGCCATTAAAACCTCCTCCTGCCAGGCTCATATACATATGAATGGAACCTCAGGAAGGATGTTAA	<u>262</u>	Human adenovirus
PBAd_00007	TTGCAACACGTAATGAAATAGGAGTGGGTAACAACCTGCCATGGAAATTAAACCTAAATGCCAACCTATG	<u>263</u>	Human adenovirus

seqid	sequence(5'-3')	SEQ ID NO:	species
PBAd_00008	TTGGGGTAAC TGACACCTATCAAGCTATTAAGGCTA ATGGCAATGGCTCAGGCATAATGGAGATATTAC	<u>264</u>	Human adenovirus
PBAd_00009	AGGTATCAAGGCATTAAAGTTAAAACCGATGACGCT AATGGATGGAAAAAGATGCTAATGTTGATACAG	<u>265</u>	Human adenovirus
PBAd_00010	GAGAAGTTTCTGTACTCCAATGTGGCTTGTACCT TCCAGATGTTACAAGTACACGCCACCTAACATT	<u>266</u>	Human adenovirus
PBAd_00011	ATCAGTCATTAAACGACTACCTCTGCAGCTAACAA TGCTTACCCCATTCCGCCATGCAACCAACAT	<u>267</u>	Human adenovirus
PBAd_00012	CTACTTCGTATATTCTGGATCTATTCCCTACCTGGAT TGGCACCTTTACCTTAACCACACTTCAGAAG	<u>268</u>	Human adenovirus
PBAd_00013	ACCTGCCAGTGGAAAGGATGCTAACAGAAAATGCAT ACCTTTGGGTAGCTGCCATGCCAGGTGTTACTG	<u>269</u>	Human adenovirus
PBAd_00014	ATAGAAGCTGATGGGCTGCCTATTAGAATAGATTCA ACTTCTGGAAC TGACACAGTAATTATGCTGATA	<u>270</u>	Human adenovirus
PBAd_00015	TTGAAATTAAAGCGCACCGTGGACGGCGAGGGGTAC ACGTGGCCAGTGCAACATGACCAAGGACTGGTT	<u>271</u>	Human adenovirus
PBAd_00016	CGGCAACGACCGGCTCCTGACGCCAACGAGTTGAA ATTAAGCGCACCGTGGACGGCGAGGGTACAAC	<u>272</u>	Human adenovirus
PBAd_00017	CTCCAGTAACTTATGTCCATGGGCGACTCACAGAAC CCTGGCCAAAACCTCTACGCCACTCCGCC	<u>273</u>	Human adenovirus
PBAd_00018	GCTAACTTCCCCTATCCGTTATAGGCAAGACCGCA GTTGACAGCATTACCCAGAAAAAGTTCTTGCG	<u>274</u>	Human adenovirus
PBAd_00019	ACAGTCCTTCCAACGTAAAAATTCTGATAACCCAA ACACCTACGACTACATGAACAAGCGAGTGGTGGC	<u>275</u>	Human adenovirus
PBAd_00020	AAGATGAACCTCCAATTACTGCTTCCACTGGGAG GTGTGATTAATACAGAGACTCTTACCAAGGTAAA	<u>276</u>	Human adenovirus
PBAd_00021	AGCTAACATGCTTACCCATCCCTGCCATGCAACCA AACATTCCAATTCCATCCATCTCGCAACTGG	<u>277</u>	Human adenovirus
PBAd_00022	TTCAACTCTTGAAAGCCATGCTGCGCAACGATAACCAATGATCAGTCATTCAACGACTACCTCTGCAAGCT	<u>278</u>	Human adenovirus
PBAd_00023	AGGCTGTGGACAGCTATGATCCCAGTGGTCTGTATTA TTGAAAATCATGGCGTCGAGGATGAACTGCTAA	<u>279</u>	Human adenovirus
PBAd_00024	TGAAATTGTGCTTACACGGAAAATGTCAATTGGA AACTCCAGACAGCCATGTGGTATAAGCCAGGA	<u>280</u>	Human adenovirus
PBAd_00025	CATCGGCTATCAGGGCTTCTACATTCCAGAAGGATA CAAAGATCGCATGTATTCACTTTTCAGAAACTTC	<u>281</u>	Human adenovirus

seqid	sequence(5'-3')	SEQ ID NO:	species
PBAd_00026	GCTGCTTCTCCAGGCCTACACTTATGAGTGGAA CTTAGGAAGGATGTGAACATGGTCTACAGAGT	<u>282</u>	Human adenovirus
PBAd_00027	ATGACACCAATGATCAGTCATTCAACGACTACCTAT CTGCAGCTAACATGCTCACCCATTCCCTGCCAA	<u>283</u>	Human adenovirus
PBAd_00028	CTTGCCAACATAAACATTGGATACCAGGGCTCTAC GTTCTGAGGGTACAAGGATCGCATGTACTCCT	<u>284</u>	Human adenovirus
PBAd_00029	GATCGCATGTACTCCTCTTCAGAAACTTCCAGGCC ATGAGTAGACAGGTGGTTGATGAGATTAAC TACA	<u>285</u>	Human adenovirus
PBAd_00030	CCCCTAAGGGCGCTCCAAATACATCTCAGTGGATTG CTGAAGGCGTAAAAAAAGAAGATGGGGATCTGA	<u>286</u>	Human adenovirus
PBAd_00031	AGAAAATGTAAATTGGAAACTCCAGATTCCATGT TGTGTTACAAAGCAGGAACCTCAGACGAAAGCTCT	<u>287</u>	Human adenovirus
PBAd_00032	TGTGGCTACCAATACTGTTACCAAGGTGTTAAGTT ACAAACTGGTCAAACGTACAAATGGCAGAAAGAT	<u>288</u>	Human adenovirus
PBAd_00033	CCGAATTGGGAAGGGTAGCGTATTCGCCATGGAAAT CAATCTCCAGGCCAACCTGTGGAAGAGTTTCTG	<u>289</u>	Human adenovirus
PBAd_00034	TTGATGAGGTCAATTACAAAGACTTCAGGCCGTG CCATACCTACCAACACAACACTCTGGCTTTGT	<u>290</u>	Human adenovirus
PBAd_00035	TGACGAAGAGGAAGAGAAAAATCTCACCACTTACAC TTTGGAAATGCCAGTGAAAGCAGAAGGTGGT	<u>291</u>	Human adenovirus
PBAd_00036	AGAAGATTTGACATTGACATGGCTTTCTTGATTC CAACACTATTAAACACACCAGATGTTGTGCTGTAT	<u>292</u>	Human adenovirus
PBS10062	CTCACATCCTAGGAAGATGCATAGTTAGATGTTA AAGGTGTAGAAGAATTGCATGACGATTAGTTAA	<u>293</u>	HCoV-OC43
PBS10063	GGATTGCCATTGCACCATAGCTCAACTCACGGATG CAGCACTGTCCATTAGGAAATGTTGATTAT	<u>294</u>	HCoV-OC43
PBS10064	GCATGCAATTCAATTATAAAATCACCATCAACCCCT CATCACCGGCTAGACTGAAATAGTTAAGCTCGG	<u>295</u>	HCoV-OC43
PBS10065	ATAGTTAGTCACTGGATGGGAATCGTTGAATAC ACATCACCCACTGATAAGCTAGCTATGATTATGG	<u>296</u>	HCoV-OC43
PBS10049	AATGGGGTTATGTTGGTCACTCTCCACTAATCACC ATGCAATTGTAATGTTAGAAATGAGCATGT	<u>297</u>	HCoV-229E
PBS10050	GTGTATGACTGCTTGTAAAGAATGTTGATGGATGGTCA ATTACCTACCCATGATAGCTAATGAAATGCCA	<u>298</u>	HCoV-229E
PBS10051	TTGCATCTCTTGTGGTATGCCATCTTTGTTG CATATGAAACAGCAAGACAAGAGTATGAAATGC	<u>299</u>	HCoV-229E

seqid	sequence(5'-3')	SEQ ID NO:	species
PBS10052	AAATGGTCCCTACCCACAAATAATCAAACAAATTGAA GAAGGCTATGAATGTTGCAAAAGCTGAGTTGAC	<u>300</u>	HCoV-229E
PBS10053	CTGCTGCAGCTATGTACAAAGAACGACGTGCTGTTA ATAGAAAATCAAAGTTGTTAGGCCATGCATAG	<u>301</u>	HCoV-229E
PBS10054	ACGTTTGGACATGTCTAGTGTTGACACTATCCTTAA TATGGCACGTAATGGTGTGTCCTCTTCCGTT	<u>302</u>	HCoV-229E
PBS10055	CTGGTGGTAAAGTTCAATTTCTGATGACGTTGAAG TAAAAGACATTGAACCTGTTACAGAGTCAGCT	<u>303</u>	HCoV-229E
PBS10056	TTTACAGAGTCAGCTTGCTTGAGTTGAAGATG AAAAACTTGTAGATGTTGTGAAAAGGCAATTGG	<u>304</u>	HCoV-229E
PBS10057	GATGTTGTGAAAAGGCAATTGCGAACAAAAATTAAA CATGAAGGTGACTGGGATAGCTTGTGTAAGACTA	<u>305</u>	HCoV-229E
PBS10058	GCGTTGTTGGCCTTTTCTTGTCTAACGATAGTGAT TTTGGTCTGGTGATCTTGTGCGATTCTTATTG	<u>306</u>	HCoV-229E
PBS10059	AGCAAGACAAGAGTATGAAAATGCTGTTGCAAATGG TTCCTCACCAACAAATAATCAAACAATTGAAGAAG	<u>307</u>	HCoV-229E
PBS10060	TTGAAGAAGGCTATGAATGTTGCAAAAGCTGAGTT GACAGGGAATCATCTGTTCAAAAGAAAATTAAACA	<u>308</u>	HCoV-229E
PBS10061	CTGCTGCAGCTATGTACAAAGAACGACGTGCTGTTA ATAGAAAATCAAAGTTGTTAGTGCCATGCATAG	<u>309</u>	HCoV-229E
PBHE_00001	CGGGATAAGGCACTCTCTATCAGAATGGATGTCTTG CTGCTATAATAGATAGAGAAGGTTAGCAGACT	<u>310</u>	Human enteric coronaviruse
PBHE_00002	CCCTCGCAGGAAAGTCGGGATAAGGCAGCTCTCTATC AGAATGGATGTCTGCTGCTATAATAGATAGAGA	<u>311</u>	Human enteric coronaviruse
PBHE_00003	ATGGATTTGAGGACGCAGAGGAGAAGTTGGACAA CCCTAGTAGTCAGAGGTGGATATAGTATGCT	<u>312</u>	Human enteric coronaviruse
PBHE_00004	CCTGGGTTATGTAAGTCGCTAAGTGTGGCGAAAAG GGTGCCTACAATAAGATCATAAACGTGTCGG	<u>313</u>	Human enteric coronaviruse
PBHE_00005	GGGGATGCTGGTTTACTAGCATACTCAGTGGTTTG TTATATGATTCAACCCTGTTTACAGCAAGG	<u>314</u>	Human enteric coronaviruse
PBHE_00006	CATGACGGCAGTTGCTGTCACCCCCGTACTGTTA TTTCGTAATTCTACTACCAACTATGTTGGTG	<u>315</u>	Human enteric coronaviruse
PBRh_00001	GGCTGAGTGATTACATCACAGGTTGGTAGAGCTT TTGGTGTGGGTTACTGACCAAATCTAACAAA	<u>316</u>	Human rhinovirus
PBRh_00002	GAAAAGCTATTAGCTTGGTAGACAGAACTACCAACG TTAGGTATAGTGTGGATCAACTGGTCACGGCTAT	<u>317</u>	Human rhinovirus

seqid	sequence(5'-3')	SEQ ID NO:	species
PBRh_00003	GGCCAAGTAATAGCTAGACATAAGGTTAGGGAGTTAACATAATCCAGTCAACACGGCAACTAAGTCAA	<u>318</u>	Human rhinovirus
PBRh_00004	GATAACAAGGGCATGTTATTCAACCAAGTAATTTGTTCTAGCCTCCACAAATTCTAACACACTAAGCCCC	<u>319</u>	Human rhinovirus
PBRh_00005	GGCCAAGAAGTAAGGTTGTGTTAGTACCACTCAGGGTTACAGTTATGTTAACACCTGGATCTGGCA	<u>320</u>	Human rhinovirus
PBRh_00006	GTAATGCGTAAGTGCAGGGATGGGACCAACTACTTTGGTGTCCGTGTTCTGTTCTTGATTGCA	<u>321</u>	Human rhinovirus
PBRh_00007	TAAAAGAGGATTTCAGAGCTGATGAGGCCACTCTTCCCTATACACCTACCTTCCTGTGGCTGAGATT	<u>322</u>	Human rhinovirus
PBRh_00008	GCAAGTTTCATCAGGGTTTATTAATAGTTGCCGCCAACATCAATTGGCATCTGCAACAAAGTGG	<u>323</u>	Human rhinovirus
PBMP_00001	ATATATGAAGGAACACCAGTGGCGAAGGCAGAAACTTAGGCCATTACTGACGCTTAGGCTTGAAAGTGTG	<u>324</u>	Mycoplasma pneumoniae
PBMP_00002	GCAGTAGGGAATTTCACAATGAGCGAAAGCTTGAAGGATGCGCTGAACGATGAAGGTCTTA	<u>325</u>	Mycoplasma pneumoniae
PBMP_00003	AACACATTAAGTATCTCGCTGGGTAGTACATTGCAAGAATGACGGGACCC	<u>326</u>	Mycoplasma pneumoniae
PBMP_00004	ACACCGTAAACGATAGATACTAGCTGTCGGGCGATCCCCTGGTAGTGAAGTTAACACATTAAGTATCT	<u>327</u>	Mycoplasma pneumoniae
PBMP_00005	ACATCCTTGGCAAAGTTATGAAACATAATGGAGGTAAACCGAGTGCAGAGTGGTGCATGGTTGTCGTCA	<u>328</u>	Mycoplasma pneumoniae
PBR_00001	TTATAACTTAACCGTCGGCAGTTGGTAAGAGACCACTGCGATCAATTGTCGAGGGCGCTGGGAAGTG	<u>329</u>	Rubella virus
PBR_00002	ATACCCAGACCTGTGTTACGCAGATGCAGGTCACTGATCACCCAGCACTCCACGCAATTGCGGGTATA	<u>330</u>	Rubella virus
PBR_00003	AGAAACTCCTAGATGAGGTTCTGGCCGGCTGGTAAGAGACCA	<u>331</u>	Rubella virus
PBR_00004	ATACCCAGACCTGTGTTACGCAGATGCAGGTCACTGATCACCCAGCACTCCACGCAATTGCGGGTATA	<u>332</u>	Rubella virus
PBR_00005	TCTTACTTCAACCCCTGGCGGCAGCTACTACAAGCAGTACACCGCTACCGCGTGCAGGTGAACCT	<u>333</u>	Rubella virus
PBM_00001	AAGGCTTGTTCAGAGATTGCAATGCATACTACTGAGGACAGGATCAGTAGAGCAGTTGGACCCAGACAA	<u>334</u>	Measles virus
PBM_00002	AGGATCAGTAGAGCAGTTGGACCCAGACAAGCCAA	<u>335</u>	Measles virus
	GTGTCATTCTACACGGTGTCAAAGTGAGAATG		

seqid	sequence(5'-3')	SEQ ID NO:	species
PBM_00003	TCAGTAGAGCAGTTGGACCCAGACAAGCCCAAGTGT CATTCCTACACGGTATCAAAGTGAGAATG	<u>336</u>	Measles virus
PBM_00004	CCCAGGGAATGTACGGGGAACTTACCTAGTTGAAA AGCCTAATCTGAGCAGCAAAGGATCAGAATTATC	<u>337</u>	Measles virus
PBM_00005	CCCAGGGAATGTACGGGGAACTTACCTAGTTGAAA AGCCTAATCTGAGCAGCAAAGGATCAGAATTATC	<u>338</u>	Measles virus
PBRSV_00001	CAAACCCACAAACAAACCAACCACCAAAACCACAAA CAAAAGAGACCCAAAACACCAGCCAAAACGACG	<u>339</u>	Human respiratory syncytial virus
PBRSV_00002	GCAGCACTTGTAAATAACCAAATTAGCAGCAGGAGAC AGATCAGGTCTTACAGCAGTAATTAGGAGGGCAA	<u>340</u>	Human respiratory syncytial virus
PBRSV_00003	CAAGAGGGGTAGTAGAGTTGAAGGAATCTTGCAG GATTGTTATGAATGCCTATGGTCAGGGCAAGT	<u>341</u>	Human respiratory syncytial virus
PBRSV_00004	GACTAACAGCAGAAGAATTGGAAGCCATAAAGAAT CAACTCAACCCCTAAAGAAGATGATGTAGAGCTTT	<u>342</u>	Human respiratory syncytial virus
PBRSV_00005	TCACAATCCACTGTGCTCGACACAACCACATTAGAA CACACAATCCAACAGCAATCCCTCCACTCAACCA	<u>343</u>	Human respiratory syncytial virus
PBRSV_00006	GACTAACAGCAGAAGAATTGGAAGCCATAAAGAAT CAACTCAACCCCTAAAGAAGATGATGTAGAGCTTT	<u>344</u>	Human respiratory syncytial virus
PBPI_00001	GCCGACGACCATCAAGCGTAGCCAACAAAGATCAGA GAGAACACAGAATTAGCAACTCCACAAATCAACA	<u>345</u>	Parainfluenza
PBPI_00002	CGACCCAAGATCATAGATCAAGTGAGGAGAGTGGAA TCTCTAGGAGAACAGGTGAGTCAAAACTGAGAC	<u>346</u>	Parainfluenza
PBPI_00003	CGAAATGAAGAGGGAAACCAAGAACACATCAGTCGA TGAGATGGCCAAGTTACTAGTAAGTCTTGGTGTA	<u>347</u>	Parainfluenza
PBPI_00004	CTCCTTGCAATGCCATACGTAGTCGGAAATTATAT CTCACTACAAACGGTGTCAATGCTGATGTCAAGT	<u>348</u>	Parainfluenza
PBPI_00005	GAACAAAAACAGATGGGTTCATGTCAAAACGAGAG ACATGGAGTATGAAAGAACACAGAGTGGTTGTT	<u>349</u>	Parainfluenza
PBPI_00006	TGTTCCAAGGGCAAAGAGAGAATGCGGATCTAGAGG CATTGCTTCAGACATATGGATATCCTGCATGTCT	<u>350</u>	Parainfluenza
PBPI_00007	GGTATATCCCTTCCCAGCCACATCATGACAAAAG GGCATTCTAGGTGGAGCAGATATCAAAGAATG	<u>351</u>	Parainfluenza

seqid	sequence(5'-3')	SEQ_ID NO:	species
PBPI_00008	GTATAACAACCACATGTACATGCAACGGTATTGGCA ATAGAATCAATCAACCACCTGATCAAGGAGTAAA	<u>352</u>	Parainfluenza
PBPI_00009	CCCAACCCATTCAAAACGAAAATCTCAAAAGAGATT GGCAACACAACAAACACTGAACATCATGCCAAC	<u>353</u>	Parainfluenza
PBME_00001	AAAAGTGTATCACAGAAGTTGTTCATTGAGTATGG CAAAGCATTAGGCTCATCATCTACAGGCAGCAAA	<u>354</u>	Human metapneumovirus
PBME_00002	GAAAGTCTATTGTTAATATATTATCATGCAAGCTTAT GGAGCCGGTCAAACAATGCTAAGGTGGGGGTCA	<u>355</u>	Human metapneumovirus
PBME_00003	ACGCTGTTGTTGGAGAAATTCTGTATGCTAACAT GCTGATTACAAATATGTCAGAAATAGGAATAC	<u>356</u>	Human metapneumovirus
PBME_00004	TTAAGGAATCATCAGGTAAATATCCCACAAAATCAGA GCCCTCAGCACCAGACACACCCATAATCTTATT	<u>357</u>	Human metapneumovirus
PBME_00005	TGAGCAATCAAAGGAGTGCAACATCAACATATCCAC TACAAATTACCCATGCAAAGTCAGCACAGGAAGA	<u>358</u>	Human metapneumovirus
PBME_00006	CTGTTCCATTGGCAGCAACAGAGTAGGGATCATCAA GCAGCTGAACAAAGGTTGCTCCTATATAACCAAC	<u>359</u>	Human metapneumovirus
PBME_00007	ACTTAATGACAGATGCTGAACTAGCCAGGGCCGTT CTAACATGCCGACATCTGCAGGACAAATAAAATT	<u>360</u>	Human metapneumovirus
PBME_00008	AAAAAAAGGAAACTATGCTTGCTCTTAAGAGAAAG ACCAAGGGTGGTATTGTCAGAATGCAGGGTCAAC	<u>361</u>	Human metapneumovirus
PBME_00009	GAAAAGAACACACCAGTTACAATACCAGCATTTATC AAATCGGTTCTATCAAAGAGAGTGAATCAGCCA	<u>362</u>	Human metapneumovirus
PBME_00010	CAAATCAGTTGGCAAAAAAACACATGATCTGATCGC ATTATGTGATTTATGGATCTAGAAAAGAACACA	<u>363</u>	Human metapneumovirus
PBME_00011	CAGCTAAAGACACTGACTATAACTACTCTGTATGCT GCATCACAAAGTGGTCCAATACTAAAGTGAATG	<u>364</u>	Human metapneumovirus
PBME_00012	AAAAGAACACACCAGTTACAATACCAGCATTATCA AATCGGTTCTATCAAAGAGAGTGAATCAGCCAC	<u>365</u>	Human metapneumovirus
PBME_00013	CTATTATAGGAGAAAAAGTGAACACTGTATCTGAAA CATTGGAATTACCTACTATCAGTAGACCCACCAA	<u>366</u>	Human metapneumovirus
PBME_00014	AAGTTAGCATGGACAGACAAAGGTGGGGCAATCAA ACTGAAGCAAAGCAAACATCAAAGTTATGGATC	<u>367</u>	Human metapneumovirus
PBME_00015	CAGGAAAATACACAAAGTTGGAGAAAGATGCTCTAG ACTTGCTTCAGACAATGAGAAGAAGATGCGAGA	<u>368</u>	Human metapneumovirus
PBME_00016	CTAATAGCAGACATAATAAGAAGCCAAGGGAAAA GCAGCAGAAATGATGAGAAGAAGAATGAACCAGC	<u>369</u>	Human metapneumovirus

seqid	sequence(5'-3')	SEQ ID NO:	species
PBCP_00001	ACCCTTATCGTTAGTTGCCAGCACTTAGGGTGGGAA CTCTAACGAGACTGCCCTGGGTTAACCAAGGAGGAA	<u>370</u>	Chlamydophila pneumoniae
PBCP_00002	ATAAGAGAGGTTGGCTAATATCCAATTGATTGAGC GTACCAAGGTAAGAACGACCGGCTAACCTCGTGC	<u>371</u>	Chlamydophila pneumoniae
PBCP_00003	CATGGGATCTTAAGTTTAGTTGAATACTTCTGGAA AGTTGAACGATAACAGGGTGTAGTCCCCTAACG	<u>372</u>	Chlamydophila pneumoniae
PBCP_00004	GGGTGCTAGCGTTAATCGGATTATTGGCGTAAAG GGCGTGTAGGCGAAAGGAAAGTTAGATGTTAAA	<u>373</u>	Chlamydophila pneumoniae
PBCP_00005	GCCAGGGACTTAAGTTAACCGCGAGATTAAGGGAT TTACATTCCGGAGTCGAAGCGAAAGCGAGTTTA	<u>374</u>	Chlamydophila pneumoniae
PBCP_00006	GCCAGGGACTTAAGTTAACCGCGAGATTAAGGGAT TTACATTCCGGAGTCGAAGCGAAAGCGAGTTTA	<u>375</u>	Chlamydophila pneumoniae

Please replace Table 16, beginning on page 38 and bridging to page 42, with a new Table 16 as follows:

Table 16. Exemplary probes for non-SARS-CoV infectious organisms damaging host's immune system

id	sequence(5'-3')	SEQ ID NO:	species
PBHAV_00001	GGTGTGAAACCTGAGAAAAATATTACACCAAACCTGTGGC CTCAGATTATTGGATGGATAGTGGAC	<u>376</u>	HAV
PBHAV_00002	ACTGAGGAGCATGAAATAATGAAGTTCTTGGAGAGGAGT GACTGCTGATACTAGGGCTTGAGAAGAT	<u>377</u>	HAV
PBHAV_00003	CATGGCGTACTAACGGCCAAACAAAGTGTAAATTGGATGC AGATCCAGTAGAGTCCCAGTCACACTCTAG	<u>378</u>	HAV
PBHAV_00004	GTGCAGTGATGGACATTACAGGAGTGCAGTCACCTTGAGA TTTCGTGTTCTGGATTCTGATAACACC	<u>379</u>	HAV
PBHAV_00005	CCAAAAGAGATTAAATTGGTGGATGAAAATGGTTGCTG TTAGGAGTTCACCCAAGATTGGCCAGAG	<u>380</u>	HAV
PBHAV_00006	AGAGATGCTTGATAGGGTAACAGCGGGGATATTGGTGA GTTGTTAACACAAAACCATTCAACGCCG	<u>381</u>	HAV
PBHBV_00001	GCTGGATGTGCTGCCGGCTTTATCATATTCTCTTCATC CTGCTGCTATGCCTCATCTCTATTGGT	<u>382</u>	HBV
PBHBV_00002	ATATACATCCTTCCATAGCTGCTAGGTTGACTGCCAACT AGATTCTCGGGACGTCTTGTCTAC	<u>383</u>	HBV
PBHBV_00003	ATTCTTTCCCGATCATCAGTTGGACCCCTGCATTGGAGCCA ATTCAAAACATCCAGATTGGGACTTCAC	<u>384</u>	HBV

<u>id</u>	<u>sequence(5'-3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PBHBV_00004	CTCATGTTGCTGTACAAAACCTACGGATGGAAATTGCACCT GTATTCCCCATCCCATCTTGGGCTTTC	<u>385</u>	HBV
PBHBV_00005	AGAGTCTAGACTCGTGGTGGACTTCTCTCAATTCTAGGG GGAGCACCCGTGTGTTGGCCAAAATTC	<u>386</u>	HBV
PBHBV_00006	CCTTGGATGGCTTGGGGCATGGACATTGACCCTTATAAAG AATTTGGAGCTACTGTGGAGTTACTCTCA	<u>387</u>	HBV
PBHCV_00001	TGGGAGACAGCAAGACACACTCCAGTCAACTCCTGGCTAGG CAACATAATCATGTTGCCAACACTGT	<u>388</u>	HCV
PBHCV_00002	TGAGCGACTTTAACGACCTGGCTGAAAGCCAAGCTCATGCCA CAACTGCCTGGATTCCCTTGTGT	<u>389</u>	HCV
PBHCV_00003	TATAGATGCCCACTTCTATCCAGACAAAGCAGAGTGGGG AGAACTTCCCTAACCTGGTAGCGTACCAA	<u>390</u>	HCV
PBHCV_00004	TAACAACACCAGGCCACCGCTGGCAATTGGTCGGTTGTA CCTGGATGAACTCAACTGGATTACCAAA	<u>391</u>	HCV
PBHCV_00005	TTTATCCCTGTGGAGAACCTAGAGACAACCATGAGATCCCC GGTGTTCACGGACAACCTCCTCCACCAAG	<u>392</u>	HCV
PBHCV_00006	TTTATCCCTGTGGAGAACCTAGAGACAACCATGAGATCCCC GGTGTTCACGGACAACCTCCTCCACCAAG	<u>393</u>	HCV
PBHDV_00001	TTCCCTTCTCTCGTCTTCTCGTCAACCTCTTAAGTTCT CTTCTTCTTGCTGAGGTGCTTCCCT	<u>394</u>	HDV
PBHDV_00002	TAAGCCCATAGCGATAGGGAGAGATGCTAGGAGTTAGAGGA GACCGAAGCGAGGAGGAAAGCAAAGAGAG	<u>395</u>	HDV
PBHDV_00003	TTGGAGAGCACTCCGCCGAAAGGTCGAGGTACCCAGAAGG AGGAATCTCACGGAGAAAAGCAGACAAAT	<u>396</u>	HDV
PBHDV_00004	TTAAGTTCCCTTCTTCTTGCTGAGGTGCTTCCCTCC CGCGGCCAGCTGCTTCTCTTGAGG	<u>397</u>	HDV
PBHDV_00005	AAAAAGAGAAAGCAAGAGACGGACGATTCCCCATGACTCT GGAGACATCCTGGAAGGGGAAAGAAGGAA	<u>398</u>	HDV
PBHDV_00006	AAGTTCCCTTCTTCTTGCTGAGGTGCTTCCCTCCCG CGGCCAGCTGCTTCTCTTGAGG	<u>399</u>	HDV
PBHGV_00001	TCATATCATGCATCATTGGACACGGCCCCCTTGCTCCAC TTGGCTTGCTGAGTGCAATGCAGAT	<u>400</u>	HGV
PBHGV_00002	TAAAGTGGAAAGTGAAGTTTGGAGATGGACTGAACAGCTG GCCTCCAACACTGGATTCTGGAATACCT	<u>401</u>	HGV
PBHGV_00003	TAGGTCGTAATCCCGGTACCTTGGTAGCCACTATAGGTG GGTCTTAAGAGAAGGTTAAGATTCCTTT	<u>402</u>	HGV

<u>id</u>	<u>sequence (5'-3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PBHGV_00004	TTCTTGGTTGCCTCCACCAGTGGTCGCGACTCGAAGATAG ATGTGTGGACTTAGTGCCAGTTGG	<u>403</u>	HGV
PBHGV_00005	TCCAACACTGGATTCTGGAATACCTCTGGAAGGTCCATT TGATTTCTGGAGAGGCGTGATAAGCCTGA	<u>404</u>	HGV
PBHGV_00006	ACGTTACCAAGGTCTTCATGTATCCCGGACAGTTACTTCA GCAAGTTGACTATTGCGACAAGGTCTCAG	<u>405</u>	HGV
PBTTV_00001	TGTCAGTAACAGGGTCGCCATAGACTTCGGCCTCCATT ACCTTGAAAAACTACCAAAATGGCCGTT	<u>406</u>	TTV
PBTTV_00002	ATGTCATCCATTCTGGGCCGGGTCTACGTCCCTCATATAA GTAAC TGCACTCCGAATGGCTGAGTTT	<u>407</u>	TTV
PBTTV_00003	GGGATCTAGCATCCTTATTCAAAATAGCACCATAAACATGT TTGGTGACCCCAAACCTTACAACCCCTTCC	<u>408</u>	TTV
PBTTV_00004	TGTTAGAAATCCCTGCAAAGAAACCCACTCCTCGGGCAATA GAGTCCCTAGAAGCTTACAAATCGTTGAC	<u>409</u>	TTV
PBTTV_00005	TCAAGGATTGACGTAAAGGTTAAAGGTATCCTCGGGCGAA GCTACACAAAATGGTGGACAACATCTTCC	<u>410</u>	TTV
PBB19_00001	GGCATGGTTAACTGGAATAATGAAAACCTTCCATTAAATGA TGTAGCAGGGAAAAGCTTGGTGGTCTGGG	<u>411</u>	B19
PBB19_00002	GGCAAGAAAAATACACTGTGGTTTATGGGCCGCAAGTAC AGGAAAACAAACTGGCAATGCCATTG	<u>412</u>	B19
PBB19_00003	GCCATTCTCATGGTCAGACCACTTATGTAACGCTGAAGA CAAAGAGTATCAGCAAGGAGTGGTAGAT	<u>413</u>	B19
PBB19_00004	AATTCGAGAATTACCCAGATTGGTGGTGTAGCTGC CATGTGGGAGCTCTAATCCCTTTCTGT	<u>414</u>	B19
PBHCMV_00001	AGGTGCGAACGCTTTATGAAGGTAAAGCCGTGGCCAG GAGATTATCCGTATCTGCATACTCGCTAA	<u>415</u>	HCMV
PBHCMV_00002	TAAACGACATGTATCTGTTGGTACGCTCGACACTGCAG CTCGCACACCGCCTGGAGCTACAAATGAT	<u>416</u>	HCMV
PBHCMV_00003	CAAAGCAGCGTCAACAAACAGCCACACAGAAACCTACGTGGA GACGACACGGGACTTTTATTGACGGAGA	<u>417</u>	HCMV
PBHCMV_00004	TGCTCCAAAGCAGCGTCAACAAACAGCCACACAGAAACCTAC GTGGAGACGACACGGGACTTTTATTGAC	<u>418</u>	HCMV
PBEBV_00001	GAGTTAAAGCAACTACTGTTTATTTCAAAATGAGCTGG GTATAGTTGATGATCTGTAGGCCAGCTC	<u>419</u>	EBV
PBEBV_00002	ACAGTGACAGTGGAGAAACACGGCCTCTGAGACATGTATG GGGGTGTTCATCTCACGCAGAAAATCTT	<u>420</u>	EBV

<u>id</u>	<u>sequence (5'-3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PBEBV_00003	TGAAGAAGTCCCGTAGTAAAAATGGGATCTGTCTACACCA TGTCTGGTGTGCCGGAACATATTGATCG	<u>421</u>	EBV
PBEBV_00004	TGAAGAAGTCCCGTAGTAAAAATGGGATCTGTCTACACCA TGTCTGGTGTGCCGGAACATATTGATCG	<u>422</u>	EBV
PBHIV1_00001	ATTATTGTCTGGTATAGTGCAGCAGCAGAACAAATTGCTGA GGGCTATTGAGGCAGAACAGCATCTGTTG	<u>423</u>	HIV1
PBHIV1_00002	GCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGA CACCAAGGAAGCTTAGACAAGATAGAGG	<u>424</u>	HIV1
PBHIV1_00003	TGTATGTAGGATCTGACTTAGAAATAGGGCAGCATAGAACAA AAATAGAGGAGCTGAGACAACATCTGTT	<u>425</u>	HIV1
PBHIV1_00004	GGAATGCTAGTTGGAGTAATAAAATCTCTGGAACAGATTGG AATCACACGACCTGGATGGAGTGGACAG	<u>426</u>	HIV1
PBTP_00001	TACCTTGAAAGACGTTACCGCCAAATGCTCATCAAAAGAA CGAGGACCATGCTGACAGCACCCCGACAA	<u>427</u>	TP
PBTP_00002	TTTCGTGATCCTTTCCCTTCTGTAGCTCAGCGTCCTTT TTATCTAATTCTCTGCACGCTCCCGAG	<u>428</u>	TP
PBTP_00003	TCTTCTGACTCGCGAAAAGGCATTACTGGAACACTATTT TAGCCATGTGGTGGCTCCCTGCTATCTTA	<u>429</u>	TP
PBTP_00004	ACCTTGAAAGACGTTACGCCAAATGCTCATCAAAAGAAC GAGGACCATGCTGACAGCACCCCGACAA	<u>430</u>	TP
PBHEV_00001	AATAATTCA CGCCGTCGCTCCTGATTATAGGTTGGAACATA ACCCAAAGATGCTTGAGGCTGCTACCGG	<u>431</u>	HEV
PBHEV_00002	TTTGTGACGGGGCGGTTTAGAGACTAATGGCCCAGAGCG CCACAATCTCTTTGATGCCAGTCAGA	<u>432</u>	HEV
PBHEV_00003	ATTTTACTAGTACTAATGGTGTGGTGAGATCGGCCGG ATAGCGCTTACCTGTTAACCTGCTGA	<u>433</u>	HEV
PBHEV_00004	AGTCCACTTACGGCTTCGACCGGCCAGTCTATGCTCT GACTCTGTGACCTGGTTAATGTAG	<u>434</u>	HEV

Please replace Table 17, beginning on page 43 and bridging to page 44, with a new Table 17 as follows:

Table 17. Exemplary probes for non-SARS-CoV coronaviridae virus

seqid	sequence (5'-3')	SEQ ID NO:
PBIBV_00001	GGTATAGTGTGGTTGCTGCTAAGGTGCTGATACTAAATCTAGATCCAAT CAGGGTACAAGAGATCCTG	<u>435</u>
PBIBV_00002	GGTATAGTGTGGTTGCTGCTAAGGTGCTGATACTAAATCTAGATCCAAT CAGGGTACAAGAGATCCTG	<u>436</u>
PBMHV_00001	CCAGCCCAAGCAAGTAACGAAGCAAAGTGCCAAGAAGTCAGGCAGAAAAT TTTAAACAAGCCTGCCAA	<u>437</u>
PBMHV_00002	TCTAAACTTAAGGATGTCTTGTCTGGCAAGAAAATGCCGGTGGCA GAAGCTCCTCTGTAAACCG	<u>438</u>
PBEQ_00001	AGGATCAAGAAAATAGATCCAATTCCGGCACTAGAACACCCACCTCTGGTGT GACATCTGATATGGCTGAT	<u>439</u>
PBEQ_00002	TTTAAAACAGCGATGGCAATCAACGCCATTGTTGCCACGCTGGTATTTT TACTACTGGGAACAGGCC	<u>440</u>
PBCA_00001	TTGGAACCTATGTCGGAGAGACTTGTACCCAAAGGAATAGTAACAAGGA TCAACAGATTGGTTATTGG	<u>441</u>
PBCA_00002	GCTGAATGTGTTCCATCTGTATCTAGCATTCTGTTGGAAGCTATTGGACT GCAAAGGAAGATGGCACC	<u>442</u>
PBFE_00001	CACCAACCTCGAACAGGAGCTAAATTGGTATGTATGTCGAGAGACTT TGTTCCAAGGGAATAGGT	<u>443</u>
PBFE_00002	GGCACTCGTGGAACCAACAATGAATCCGAACCATTGAGATTGATGGTAAG ATACCACCAATTCCAGC	<u>444</u>
PBPEDV_00001	CTGATCCAAATGTTGAGCTTCTGTCACAGGTGGATGCATTAAAATG GGAATGCAAAACCCAGAG	<u>445</u>
PBPEDV_00002	ATGAGCAAATTGCGTGGCGTATGCGCCGTGGTGAAGCGAATTGAACAACCTT CAAATTGGCATTCTACTA	<u>446</u>
PBPTGV_00001	GAGAGACTTTGTACCCAAAGGAATAGGTAAACAGGGATCAACAGATTGGTTA TTGGAATAGACAAACTCGC	<u>447</u>
PBPTGV_00002	GATGGTGACCAAGATAGAAGTCACGTTCACACACAAATACCAACTTGCCAAAG GATGATCCTAAACTGGAC	<u>448</u>
PBBOV_00001	TATTTTACTATCTGGAACAGGACCGCATGCCAAAGACCAAGTATGGCACC GACATTGACGGAGTCTACT	<u>449</u>
PBBOV_00002	AGAACCCCTACCTCTGGTGTAAACACCTGATATGGCTGATCAAATTGCTAGT CTTGTCTGGCTAAACTTG	<u>450</u>
PBFIPV_00001	GAGTGTGGTTAATCAACAGGTGAAGCGCTGAGTCAACTTACCAAGTCAGTT ACAGAAAAACTTCCAGGCT	<u>451</u>
PBFIPV_00002	CCGGCATTGTAGATGGAATAAGATGGCATGTACACAGCATCTTAATTG GAGGTATGGCTTGGGCTC	<u>452</u>

seqid	sequence (5'-3')	SEQ ID NO:
PBR_00001	AAATGTTAAAACCTGGAACCTAGTGATCCACAGTTCCCCATTCTGCAGAGT TGGCCCCAACACCTGGTGC	<u>453</u>
PBR_00002	CCCATTACTCTGGTTTCGGCATTACCAATTCAAAAGGAAAGGAGT TCCAGTTGCAGATGGCA	<u>454</u>
PBPHEV_00001	TAGTAACCAGGCTGATATTAATACCCGGCTGACATGTCGATCGGGATCC AAGTAGCGATGAGGCTATT	<u>455</u>
PBPHEV_00002	TTCTTTAAAACAGCCGATGGCAATCAGCGTCAACTGCTGCCACGATGGTA CTTTACTACCTGGGAACA	<u>456</u>
PBPV_00001	GTGGTTCCCCATTACTCCTGGTTCTGGCATTACCAATTCCAGAAGGGA AAGGAGTTAAGTTGCAG	<u>457</u>
PBPV_00002	AAGAAGTCAGGCAGAAAATTAAACAAGCCTCGCCAAAAGAGGACTCCA ACAAGCAGTGCCAGTGCA	<u>458</u>
PBTK_00001	TTTGGTGATGACAAGATGAATGAGGAAGGTATTAAGGATGGCGTGTACG GCAATGCTCAACCTAGTCC	<u>459</u>
PBTK_00002	TTTGGTGATGACAAGATGAATGAGGAAGGTATTAAGGATGGCGTGTACG GCAATGCTCAACCTAGTCC	<u>460</u>
PBSDAV_00001	AGCCTGCCTCTACTGTAAAACCTGATATGCCGAAGAAATTGCTGCTCTTG TTTGGCTAAGCTAGGCAA	<u>461</u>
PBSDAV_00002	CCCCATTCTGCAGAGTTGGCCCAACACCTGGTGCTTCTTGGATC TAAATTAGAATTGGTCAA	<u>462</u>

Please replace Table 18, beginning on page 50 and bridging to page 54, with a new Table 18 as follows:

Table 18. Exemplary SARS-CoV primers

id	sequence (5'-3')	SEQ ID NO:	region
PMSL_00005	CACGTCTCCAAATGCTTGAGTGACG	<u>463</u>	SARS-CoV Nucleocapsid gene
PMSU_00006	CCTCGAGGCCAGGGCGTTCC	<u>464</u>	SARS-CoV Nucleocapsid gene
PMV_00039	TCACTTGCTTCCGTTGAGGTGGGGACCAAGACC TAATCAGA	<u>465</u>	SARS-CoV Nucleocapsid gene
PMV_00040	GGTTTCGGATGTTACAGCGTAGCCGCAGGAAGAA GAGTCACAG	<u>466</u>	SARS-CoV Nucleocapsid gene
PMV_00041	TCACTTGCTTCCGTTGAGGAGGCCAGGGCGTTCC AATC	<u>467</u>	SARS-CoV Nucleocapsid gene

<u>Id</u>	<u>Sequence (5' -3')</u>	<u>SEQ ID NO:</u>	<u>region</u>
PMV_00042	GGTTTCGGATGTTACAGCGTCAATAGCGCGAGGG CAGTTTC	<u>468</u>	SARS-Cov Nucleocapsid gene
PMV_00043	TCACTTGCTTCCGTTGAGGGGCACCCGCAATCCT AATAACAA	<u>469</u>	SARS-Cov Nucleocapsid gene
PMV_00044	GGTTTCGGATGTTACAGCGTAGCCGCAGGAAGAA GAGTCACAG	<u>470</u>	SARS-Cov Nucleocapsid gene
PMV_00090	TCGGGGACCAAGACCTAATCAGA	<u>471</u>	SARS-Cov Nucleocapsid gene
PMV_00091	AGCCGCAGGAAGAAGAGTCACAG	<u>472</u>	SARS-Cov Nucleocapsid gene
PMV_00092	AGGCCAGGGCGTTCCAATC	<u>473</u>	SARS-Cov Nucleocapsid gene
PMV_00093	CAATAGCGCGAGGGCAGTTTC	<u>474</u>	SARS-Cov Nucleocapsid gene
PMV_00094	GGCACCCGCAATCCTAATAACAA	<u>475</u>	SARS-Cov Nucleocapsid gene
PMV_00095	AGCCGCAGGAAGAAGAGTCACAG	<u>476</u>	SARS-Cov Nucleocapsid gene
PMSL_00001	ACATCACAGCTCTACACCCGTTAAGGT	<u>477</u>	SARS-Cov Replicase 1A
PMSL_00002	ATACAGAATACATAGATTGCTGTTATCC	<u>478</u>	SARS-Cov Replicase 1A
PMSU_00002	GCATCGTTGACTATGGTGTCCGATTCT	<u>479</u>	SARS-Cov Replicase 1A
PMSU_00003	GCTGCATTGGTTGTTATCGTTATGC	<u>480</u>	SARS-Cov Replicase 1A
PMV_00023	TCACTTGCTTCCGTTGAGGGAGCCGCTTGTCAACAA TGCCAATT	<u>481</u>	SARS-Cov Replicase 1A
PMV_00024	GGTTTCGGATGTTACAGCGTCATCACCAAGCTCG CCAACAGTT	<u>482</u>	SARS-Cov Replicase 1A
PMV_00025	TCACTTGCTTCCGTTGAGGGAGGTGCCATCATT TGGCATCTT	<u>483</u>	SARS-Cov Replicase 1A
PMV_00026	GGTTTCGGATGTTACAGCGTCTTGCGCCAGCGA TAGTGACTT	<u>484</u>	SARS-Cov Replicase 1A
PMV_00027	TCACTTGCTTCCGTTGAGGTGCCACCGTTCT GCAATGG	<u>485</u>	SARS-Cov Replicase 1A

<u>id</u>	<u>sequence (5'-3')</u>	<u>SEQ ID NO:</u>	<u>region</u>
PMV_00028	GGTTTCGGATGTTACAGCGTTGGGCAGCTGACA CGAATGTAGA	<u>486</u>	SARS-Cov Replicase 1A
PMV_00029	TCACTTGCTTCCGTTGAGGGAATGGCGATGTAGT GGCTATTGA	<u>487</u>	SARS-Cov Replicase 1A
PMV_00030	GGTTTCGGATGTTACAGCGTTAACGCCGGCATCC AAACATAAT	<u>488</u>	SARS-Cov Replicase 1A
PMV_00031	TCACTTGCTTCCGTTGAGGTAGCCAGCGTGGTGG TTCATACAA	<u>489</u>	SARS-Cov Replicase 1A
PMV_00032	GGTTTCGGATGTTACAGCGTCTCCCGCAGAAAG CTGTAAGCT	<u>490</u>	SARS-Cov Replicase 1A
PMV_00033	TCACTTGCTTCCGTTGAGGTATAGAGCCCGTGC GGTGATGC	<u>491</u>	SARS-Cov Replicase 1A
PMV_00034	GGTTTCGGATGTTACAGCGTATGCCATTCAAGT CTGGGAAGAA	<u>492</u>	SARS-Cov Replicase 1A
PMV_00035	TCACTTGCTTCCGTTGAGGTGGCTCAGGCCATAC TGGCATTAC	<u>493</u>	SARS-Cov Replicase 1A
PMV_00036	GGTTTCGGATGTTACAGCGTTTGCGCCAGCGAT AGTGACTTG	<u>494</u>	SARS-Cov Replicase 1A
PMV_00037	TCACTTGCTTCCGTTGAGGTCCCCTCAGGCAAA GTTGAAGG	<u>495</u>	SARS-Cov Replicase 1A
PMV_00038	GGTTTCGGATGTTACAGCGTGACGGCAATTCTG TTTGAGCAGA	<u>496</u>	SARS-Cov Replicase 1A
PMV_00074	AGCCGCTTGTCAACAATGCCAATT	<u>497</u>	SARS-Cov Replicase 1A
PMV_00075	CATCACCAAGCTGCCAACAGTT	<u>498</u>	SARS-Cov Replicase 1A
PMV_00076	AGGTTGCCATCATTTGGCATCTT	<u>499</u>	SARS-Cov Replicase 1A
PMV_00077	CTTTGCGCCAGCGATAGTGACTT	<u>500</u>	SARS-Cov Replicase 1A
PMV_00078	ATGGCACCCGTTCTGCAATGG	<u>501</u>	SARS-Cov Replicase 1A
PMV_00079	TCGGGCAGCTGACACGAATGTAGA	<u>502</u>	SARS-Cov Replicase 1A
PMV_00080	GAATGGCGATGTAGTGGCTATTGA	<u>503</u>	SARS-Cov Replicase 1A

id	sequence (5' -3')	SEQ ID NO:	region
PMV_00081	TAATGCCGGCATCCAAACATAAT	504	SARS-Cov Replicase 1A
PMV_00082	TAGCCAGCGTGGTGGTTCATACAA	505	SARS-Cov Replicase 1A
PMV_00083	CTCCCGGCAGAAAGCTGTAAGCT	506	SARS-Cov Replicase 1A
PMV_00084	TATAGAGCCCGTGCTGGTGATGC	507	SARS-Cov Replicase 1A
PMV_00085	ATCGCCATTCAAGTCTGGGAAGAA	508	SARS-Cov Replicase 1A
PMV_00086	TGGCTCAGGCCATACTGGCATTAC	509	SARS-Cov Replicase 1A
PMV_00087	TTTGCGCCAGCGATAGTGACTTG	510	SARS-Cov Replicase 1A
PMV_00088	TTCCCGTCAGGCAAAGTTGAAGG	511	SARS-Cov Replicase 1A
PMV_00089	GACGGCAATTCCCTGTTGAGCAGA	512	SARS-Cov Replicase 1A
PMV_00003	TCACTTGCTTCCGTTGAGGATGAATTACCAAGTC AATGGTTAC	513	SARS-Cov Replicase 1B
PMV_00004	GGTTTCGGATGTTACAGCGTATAACCAGTCGGTA CAGCTAC	514	SARS-Cov Replicase 1B
PMV_00005	TCACTTGCTTCCGTTGAGGGAAGCTATTGTCAC GTTCG	515	SARS-Cov Replicase 1B
PMV_00006	GGTTTCGGATGTTACAGCGTCTGTAGAAAATCCT AGCTGGAG	516	SARS-Cov Replicase 1B
PMV_00007	TCACTTGCTTCCGTTGAGGCCTCTCTTGTTCTG CTCGCA	517	SARS-Cov Replicase 1B
PMV_00008	GGTTTCGGATGTTACAGCGTGTGAGCCGCCACAC ATG	518	SARS-Cov Replicase 1B
PMV_00009	TCACTTGCTTCCGTTGAGGCTAACATGCTTAGGA TAATGG	519	SARS-Cov Replicase 1B
PMV_00010	GGTTTCGGATGTTACAGCGTCAGGTAAAGCGTAAA ACTCATC	520	SARS-Cov Replicase 1B
PMV_00011	TCACTTGCTTCCGTTGAGGGCCTCTCTTGTTCTT GCTCGC	521	SARS-Cov Replicase 1B

<u>id</u>	<u>sequence (5'→3')</u>	<u>SEQ ID NO:</u>	<u>region</u>
PMV_00013	TCACTTGCTTCCGTTGAGGCACCGTTCTACAGG TTAGCTAACGA	522	SARS-Cov Replicase 1B
PMV_00014	GGTTTCGGATGTTACAGCGTAAATGTTACGCAG GTAAGCGTAAAA	523	SARS-Cov Replicase 1B
PMV_00015	TCACTTGCTTCCGTTGAGGTACACACCTCAGCGT TG	524	SARS-Cov Replicase 1B
PMV_00016	GGTTTCGGATGTTACAGCGTCACGAACGTGACGA AT	525	SARS-Cov Replicase 1B
PMV_00017	TCACTTGCTTCCGTTGAGGGCTTAGGATAATGCC CTCTC	526	SARS-Cov Replicase 1B
PMV_00018	GGTTTCGGATGTTACAGCGTCCACGAATTATGA TCAACATCCC	527	SARS-Cov Replicase 1B
PMV_00019	TCACTTGCTTCCGTTGAGGGCTCGCAAACATAAC ACTTGC	528	SARS-Cov Replicase 1B
PMV_00020	GGTTTCGGATGTTACAGCGTGAGACACTCATAGA GCCTGTG	529	SARS-Cov Replicase 1B
PMV_00055	ATGAATTACCAAGTCAATGGTTAC	530	SARS-Cov Replicase 1B
PMV_00056	ATAACCAGTCGGTACAGCTAC	531	SARS-Cov Replicase 1B
PMV_00057	GAAGCTATTCGTCACGTTCG	532	SARS-Cov Replicase 1B
PMV_00058	CTGTAGAAAATCCTAGCTGGAG	533	SARS-Cov Replicase 1B
PMV_00059	CCTCTTTGTTCTTGCTCGCA	534	SARS-Cov Replicase 1B
PMV_00060	GTGAGCCGCCACACATG	535	SARS-Cov Replicase 1B
PMV_00061	CTAACATGCTTAGGATAATGG	536	SARS-Cov Replicase 1B
PMV_00062	CAGGTAAGCGTAAAACATC	537	SARS-Cov Replicase 1B
PMV_00063	GCCTCTCTTGTTCTTGCTCGC	538	SARS-Cov Replicase 1B
PMV_00064	CACCGTTCTACAGGTTAGCTAACGA	539	SARS-Cov Replicase 1B

<u>Id</u>	<u>sequence (5'-3')</u>	<u>SEQ ID NO:</u>	<u>region</u>
PMV_00065	AAATGTTTACGCAGGTAAGCGTAAA	<u>540</u>	SARS-Cov Replicase 1B
PMV_00066	TACACACCTCAGCGTTG	<u>541</u>	SARS-Cov Replicase 1B
PMV_00067	CACGAACGTGACGAAT	<u>542</u>	SARS-Cov Replicase 1B
PMV_00068	GCTTAGGATAATGGCCTCTC	<u>543</u>	SARS-Cov Replicase 1B
PMV_00069	CCACGAATTCTATGATCAACATCCC	<u>544</u>	SARS-Cov Replicase 1B
PMV_00070	GCTCGCAAACATAACACTTGC	<u>545</u>	SARS-Cov Replicase 1B
PMV_00071	GAGACACTCATAGAGCCTGTG	<u>546</u>	SARS-Cov Replicase 1B
PMSL_00003	CCAGCTCCAATAGGAATGTCGCACTC	<u>547</u>	SARS-Cov Spike glycoprotein gene
PMSL_00004	TCCGCAGATGTACATATTACAATCTACG	<u>548</u>	SARS-Cov Spike glycoprotein gene
PMSU_00005	TTAAATGCACCGGCCACGGTTTG	<u>549</u>	SARS-Cov Spike glycoprotein gene
PMV_000100	ATAGCGCCAGGACAAACTGGTGT	<u>550</u>	SARS-Cov Spike glycoprotein gene
PMV_000101	TATATGCGCCAAGCTGGTGTGAGT	<u>551</u>	SARS-Cov Spike glycoprotein gene
PMV_000102	CGAGGCAGGAGGTACAAATTGACAG	<u>552</u>	SARS-Cov Spike glycoprotein gene
PMV_000103	ATGAAGCCGAGCCAAACATACCAA	<u>553</u>	SARS-Cov Spike glycoprotein gene
PMV_00045	TCACTTGCTTCCGTTGAGGATGCACCGGCCACGG TTTGTG	<u>554</u>	SARS-Cov Spike glycoprotein gene
PMV_00046	GGTTTCGGATGTTACAGCGTATGCCCAAGCTGG TGTGAGTTGA	<u>555</u>	SARS-Cov Spike glycoprotein gene
PMV_00047	TCACTTGCTTCCGTTGAGGTGCTGGCGCTGCTCT TCAAATACC	<u>556</u>	SARS-Cov Spike glycoprotein gene
PMV_00048	GGTTTCGGATGTTACAGCGTCGGGCTGCTTGTG GGAAGG	<u>557</u>	SARS-Cov Spike glycoprotein gene

<u>id</u>	<u>sequence (5'-3')</u>	<u>SEQ ID NO:</u>	<u>region</u>
PMV_00049	TCACTTGCTTCGTTGAGGATAGGCCAGGACAA ACTGGTGT	<u>558</u>	SARS-CoV Spike glycoprotein gene
PMV_00050	GGTTTCGGATGTTACAGCGTTATATGCGCCAAGC TGGTGTGAGT	<u>559</u>	SARS-CoV Spike glycoprotein gene
PMV_00051	TCACTTGCTTCGTTGAGGCGAGGCCGGAGGTACA AATTGACAG	<u>560</u>	SARS-CoV Spike glycoprotein gene
PMV_00052	GGTTTCGGATGTTACAGCGTATGAAGCCGAGCCA AACATACCAA	<u>561</u>	SARS-CoV Spike glycoprotein gene
PMV_00096	ATGCACCGGCCACGGTTGT	<u>562</u>	SARS-CoV Spike glycoprotein gene
PMV_00097	ATGCGCCAAGCTGGTGTGAGTTGA	<u>563</u>	SARS-CoV Spike glycoprotein gene
PMV_00098	TGCTGGCGCTGCTCTTCAAATACC	<u>564</u>	SARS-CoV Spike glycoprotein gene
PMV_00099	CGGGGCTGCTTGTGGGAAGG	<u>565</u>	SARS-CoV Spike glycoprotein gene

Please replace Table 19, beginning on page 54 and bridging to page 61, with a new Table 19 as follows:

Table 19. Exemplary primers for non-SARS-CoV infectious organism causing SARS-like symptoms

<u>id</u>	<u>Sequence (5' - 3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PMIA_00001	TTTGTGCGACAATGCTTCA	<u>566</u>	Influenza A virus
PMIA_00002	GACATTTGAGAAAGCTTGC	<u>567</u>	Influenza A virus
PMIA_00003	AGGGACAACCTNGAACCTGG	<u>568</u>	Influenza A virus
PMIA_00004	AGGAGTTGAACCAAGACGCATT	<u>569</u>	Influenza A virus
PMIA_00005	ACCACATTCCCTTATACTGGAG	<u>570</u>	Influenza A virus
PMIA_00006	TTAGTCATCATCTTCTCACAA	<u>571</u>	Influenza A virus
PMIA_00007	ACAAATTGCTCAAATGAGAAC	<u>572</u>	Influenza A virus
PMIA_00008	TGTCTCCGAAGAAATAAGATCC	<u>573</u>	Influenza A virus
PMIA_00009	GCGCAGAGACTTGAAGATGT	<u>574</u>	Influenza A virus
PMIA_00010	CCTTCCGTAGAAGGCCCT	<u>575</u>	Influenza A virus

<u>id</u>	<u>Sequence (5' - 3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PMIB_00001	CACAATGGCAGAATTTAGTGA	576	Influenza B virus
PMIB_00002	GTCAGTTGATCCCGTAGTG	577	Influenza B virus
PMIB_00003	CAGATCCCAGAGTGGACTCA	578	Influenza B virus
PMIB_00004	TGTATTACCCAAGGGTTGTTAC	579	Influenza B virus
PMIB_00005	GATCAGCATGACAGTAACAGGA	580	Influenza B virus
PMIB_00006	ATGTTCGGTAAAAGTCGTTTAT	581	Influenza B virus
PMIB_00007	CCACAGGGGAGATTCCAAAG	582	Influenza B virus
PMIB_00008	GACATTCTCCTGATTCTATAATC	583	Influenza B virus
PMIB_00009	CAAACAACGGTAGACCAATATA	584	Influenza B virus
PMIB_00010	AGGTTCACTATCTATCACAGTCTT	585	Influenza B virus
PMIB_00011	ATGTCCAACATGGATATTGAC	586	Influenza B virus
PMIB_00012	GCTCTCCTATAAATCGAATG	587	Influenza B virus
PMIB_00013	TGATCAAGTGATCGGAAGTAG	588	Influenza B virus
PMIB_00014	GATGGTCTGCTTAATTGGAA	589	Influenza B virus
PMIB_00015	ACAGAAGATGGAGAAGGCAA	590	Influenza B virus
PMIB_00016	ATTGTTCTTGGCCTGGAT	591	Influenza B virus
PMAd1_00001	TGGCGGTATAGGGGTAAC TG	592	Human adenovirus
PMAd1_00002	ATTGCGGTGATGGTTAAAGG	593	Human adenovirus
PMAd1_00003	TTTGCCGATCCCAC TTATC	594	Human adenovirus
PMAd1_00004	GCAAGTCTACCACGGCATTT	595	Human adenovirus
PMAd2_00001	CTCCGTTATCGCTCCATGTT	596	Human adenovirus
PMAd2_00002	AAGGACTGGTCGTTGGTGTC	597	Human adenovirus
PMAd2_00003	AAATGCCGTGGTAGATTTC	598	Human adenovirus
PMAd2_00004	GTTGAAGGGGTTGACGTTGT	599	Human adenovirus
PMAd3_00001	TCCTCTGGATGGCATAGGAC	600	Human adenovirus
PMAd3_00002	TGTTGGTGTAGGGCAAA	601	Human adenovirus

<u>id</u>	<u>Sequence (5' - 3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PMAd3_00003	ACATGGTCCTGCAAAGTTCC	<u>602</u>	Human adenovirus
PMAd3_00004	GCATTGTGCCACGTTGTATC	<u>603</u>	Human adenovirus
PMAd4_00001	CGCTTCGGAGTACCTCAGTC	<u>604</u>	Human adenovirus
PMAd4_00002	CTGCATCATTGGTGTCAACC	<u>605</u>	Human adenovirus
PMAd4_00003	GGCACCTTTACCTCAACCA	<u>606</u>	Human adenovirus
PMAd4_00004	TCTGGACCAAGAACCAAGTCC	<u>607</u>	Human adenovirus
PMAd5_00001	GGCCTACCCCTGCTAACCTCC	<u>608</u>	Human adenovirus
PMAd5_00002	ATAAAAGAAGGGTGGGCTCGT	<u>609</u>	Human adenovirus
PMAd5_00003	ATCGCAGTTGAATGCTGTTG	<u>610</u>	Human adenovirus
PMAd5_00004	GTTGAAGGGGTTGACGTTGT	<u>611</u>	Human adenovirus
PMAd7_00001	ACATGGTCCTGCAAAGTTCC	<u>612</u>	Human adenovirus
PMAd7_00002	GATCGAACCCCTGATCCAAGA	<u>613</u>	Human adenovirus
PMAd7_00003	AACACCAACCGAAGGAGATG	<u>614</u>	Human adenovirus
PMAd7_00004	CCTATGCCATCCAGAGGAAA	<u>615</u>	Human adenovirus
PMAd11_00001	CAGATGCTGCCAACTACAA	<u>616</u>	Human adenovirus
PMAd11_00002	AGCCATGTAACCCACAAAGC	<u>617</u>	Human adenovirus
PMAd11_00003	ACGGACGTTATGTGCCTTTC	<u>618</u>	Human adenovirus
PMAd11_00004	GGGAATATTGGTTGCATTGG	<u>619</u>	Human adenovirus
PMAd21_00001	ACTGGTTCTGGTCCAGATG	<u>620</u>	Human adenovirus
PMAd21_00002	AGCCATGTAACCCACAAAGC	<u>621</u>	Human adenovirus
PMAd21_00003	CTGGATATGGCCAGCACTTT	<u>622</u>	Human adenovirus
PMAd21_00004	CACCTGAGGTTCTGGTTGGT	<u>623</u>	Human adenovirus
PMAd23_00001	TAATGAAAAGGGCGGACAAG	<u>624</u>	Human adenovirus
PMAd23_00002	GCCAATGTAGTTGGCCTGT	<u>625</u>	Human adenovirus
PMAd23_00003	AACTCCCGCGGTAGACAGCTA	<u>626</u>	Human adenovirus
PMAd23_00004	CGTAGGTGTTGGTGTGGTG	<u>627</u>	Human adenovirus

id	Sequence (5' - 3')	SEQ ID NO:	species
PMV_a0061	TCACTTGCTTCCGTTGAGGTTGGGTGATGG GTTTCAGATTAA	<u>628</u>	HCoV-OC43
PMV_a0062	GGTTTCGGATGTTACAGCGTCTCGGAAGAT CGCCTTCTTCTA	<u>629</u>	HCoV-OC43
PMV_b0061	TTGGGGTGTAGGGTTTCAGATTAA	<u>630</u>	HCoV-OC43
PMV_b0062	CTCGGGAAAGATCGCCTTCTTCTA	<u>631</u>	HCoV-OC43
PMV_a0053	TCACTTGCTTCCGTTGAGGTTGGCTGGCGG TTTAGAGTTGA	<u>632</u>	HCoV-229E
PMV_a0054	GGTTTCGGATGTTACAGCGTGTGCGACCGCC CTTGTATGG	<u>633</u>	HCoV-229E
PMV_a0055	TCACTTGCTTCCGTTGAGGGCGTTGTTGCC TTTTCTTGTCT	<u>634</u>	HCoV-229E
PMV_a0056	GGTTTCGGATGTTACAGCGTGCCCGGCATTA TTTCATTGTTCTG	<u>635</u>	HCoV-229E
PMV_a0057	TCACTTGCTTCCGTTGAGGACAAAAGCCGCT GGTGGTAAAG	<u>636</u>	HCoV-229E
PMV_a0058	GGTTTCGGATGTTACAGCGTCAGAAATCATA ACGGGCAAATCA	<u>637</u>	HCoV-229E
PMV_a0059	TCACTTGCTTCCGTTGAGGAAGAGTTATTGC TGGCGTTGTTGG	<u>638</u>	HCoV-229E
PMV_a0060	GGTTTCGGATGTTACAGCGTGCCCGGCATTA TTTCATTGTTCTG	<u>639</u>	HCoV-229E
PMV_b0053	TTGGGCTGGCGGTTAGAGTTGA	<u>640</u>	HCoV-229E
PMV_b0054	GTGCGACCGCCCTTGTATGG	<u>641</u>	HCoV-229E
PMV_b0055	GCGTTGTTGGCCTTTCTGTCT	<u>642</u>	HCoV-229E
PMV_b0056	GCCCGGCATTATTCATTGTTCTG	<u>643</u>	HCoV-229E
PMV_b0057	ACAAAAGCCGCTGGTGGTAAAG	<u>644</u>	HCoV-229E
PMV_b0058	CAGAAATCATAACGGGCAAATCA	<u>645</u>	HCoV-229E
PMV_b0059	AAGAGTTATTGCTGGCGTTGTTGG	<u>646</u>	HCoV-229E
PMV_b0060	GCCCGGCATTATTCATTGTTCTG	<u>647</u>	HCoV-229E
PMHE_00001	GGTGGTAACCCCTCGCAGGA	<u>648</u>	Human enteric coronaviruse

<u>id</u>	<u>Sequence (5' - 3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PMHE_00002	TGGCTCTCCCTTGGGCACT	<u>649</u>	Human enteric coronaviruse
PMHE_00003	GAGAATGAACCTTATGTCGGCACCTG	<u>650</u>	Human enteric coronaviruse
PMHE_00004	TTCCGCAAGTCTTCACTTCTCAA	<u>651</u>	Human enteric coronaviruse
PMHE_00005	CAGCTTCAGCCAGGGACGTGT	<u>652</u>	Human enteric coronaviruse
PMHE_00006	TTTCCAGCTTTGCGCAGTGGT	<u>653</u>	Human enteric coronaviruse
PMHE_00007	TCTGTTTGGTGCAGGTCAATTGTG	<u>654</u>	Human enteric coronaviruse
PMHE_00008	ATGAACCAGGTCGTAAGCATCCTCAA	<u>655</u>	Human enteric coronaviruse
PMHE_00009	GTTGCTTGTCAACCCCCGTACTGTTA	<u>656</u>	Human enteric coronaviruse
PMHE_00010	AGGACACCTGCCATAGGGTAGAGAG	<u>657</u>	Human enteric coronaviruse
PMHE_00011	GGTTGTTGACTCGCGGTGGA	<u>658</u>	Human enteric coronaviruse
PMHE_00012	GGGGTAGAGAGGCCAACACTGC	<u>659</u>	Human enteric coronaviruse
PMRh_00001	ACATGGTCCCATTGGATTGT	<u>660</u>	Human rhinovirus
PMRh_00002	TGAGGAAATCTTCGCCACT	<u>661</u>	Human rhinovirus
PMRh_00003	ATGTTGCCCTAGTCTGTG	<u>662</u>	Human rhinovirus
PMRh_00004	TTCTGAAGGTGGTGTGTTGC	<u>663</u>	Human rhinovirus
PMRh_00005	TGGTATTCTGTTGGCGGTA	<u>664</u>	Human rhinovirus
PMRh_00006	ACAGCAGGTTCTTGTCAACC	<u>665</u>	Human rhinovirus
PMRh_00007	TCTTGCCTCCAATGGCTAGT	<u>666</u>	Human rhinovirus
PMRh_00008	TGACATGCCTGCATTGAGTT	<u>667</u>	Human rhinovirus
PMRh_00009	TCCCAATATGCCCTTTCAG	<u>668</u>	Human rhinovirus
PMRh_00010	CGCTGATGGGGATTGAGTAT	<u>669</u>	Human rhinovirus

<u>id</u>	<u>Sequence (5' - 3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PMRh_00011	TGTGCTCAGTGTGCTTCCTC	670	Human rhinovirus
PMRh_00012	TGCACCCATGATGACAATCT	671	Human rhinovirus
PMRh_00013	GCAGTTCTGCCAAAGAAGG	672	Human rhinovirus
PMRh_00014	TGAAGGGTTTTGGTCCATC	673	Human rhinovirus
PMRh_00015	TGCCTGATGCCCTTAAAAAC	674	Human rhinovirus
PMRh_00016	GGGTGTGATTGTACCCGACT	675	Human rhinovirus
PMMP_00001	CTAACAGTTGTATGCATTGGAACT	676	Mycoplasma pneumoniae
PMMP_00002	GTTCACGGTGTGGACTACTAGGGTAT	677	Mycoplasma pneumoniae
PMMP_00003	CTATGCTGAGAAGTAGAATAGCCACA	678	Mycoplasma pneumoniae
PMMP_00004	TGGTACAGTCAAACTCTAGCCATTAC	679	Mycoplasma pneumoniae
PMMP_00005	ATACCTAGTAGTCCACACCGTAAAC	680	Mycoplasma pneumoniae
PMMP_00006	ATGTCAAGTCTAGGTAAGGTTTCG	681	Mycoplasma pneumoniae
PMMP_00007	AGGCAGAAACTTAGGCCATT	682	Mycoplasma pneumoniae
PMMP_00008	CCGTCAATTCCGTTGAGTT	683	Mycoplasma pneumoniae
PMMP_00009	CGACGGTACACGAAAAACCT	684	Mycoplasma pneumoniae
PMMP_00010	TCCCTTCCTTCCTCCAATTT	685	Mycoplasma pneumoniae
PMR_00001	ATTCCCATGGAGAAACTCCTAGAT	686	Rubella virus
PMR_00002	GTGATCACTGACCTGCATCTG	687	Rubella virus
PMR_00003	GTAAGAGACCACGTCCGATCAAT	688	Rubella virus
PMR_00004	GAGGACGTGTAGGGCTTCTTAG	689	Rubella virus
PMR_00005	ATCGGACCTCGCTTAGGACT	690	Rubella virus
PMR_00006	CTGGGTATCACGGCTACGAT	691	Rubella virus

id	Sequence (5' - 3')	SEQ ID NO:	species
PMR_00007	AGAGACCACGTCCGATCAAT	692	Rubella virus
PMR_00008	TGAGGACGTGTAGGGCTTCT	693	Rubella virus
PMR_00009	GTCAACGCCTACTCCTCTGG	694	Rubella virus
PMR_00010	GTCTTGTGAGGGTGCTGGAC	695	Rubella virus
PMM_00001	CACATTGGCATCTGAACTCG	696	Measles virus
PMM_00002	TCTGTTGACCCTCCTGTCC	697	Measles virus
PMM_00003	AGATTGCAATGCATACTACTGAGGAC	698	Measles virus
PMM_00004	ATGCAGTGTCAATGTCTAGAGGTG	699	Measles virus
PMM_00005	CAATGCATACTACTGAGGACAGGA	700	Measles virus
PMM_00006	ATGCAGTGTCAATGTCTAGAGGTG	701	Measles virus
PMM_00007	TACCATCAGAGGTCAATTCTCAAA	702	Measles virus
PMM_00008	CTACTTCAAACACTCGGTACATGC	703	Measles virus
PMM_00009	CATGTCGCTGTCTCTGTTAGACTT	704	Measles virus
PMM_00010	CAAGCCTGGATTCTTATAACACC	705	Measles virus
PMRSV_00001	AAACCAAAGAAGAACCAACCAT	706	Human respiratory syncytial virus
PMRSV_00002	TGTTCTAATGTGGTTGTGTCGAG	707	Human respiratory syncytial virus
PMRSV_00003	TGCTAAAAGAGATGGGAGAAGTG	708	Human respiratory syncytial virus
PMRSV_00004	ATCCTTGGTATGAGACCCTTGT	709	Human respiratory syncytial virus
PMRSV_00005	ACAAGGGTCTCATACCAAAGGAT	710	Human respiratory syncytial virus
PMRSV_00006	GCTAAAACCCCCATCTTAGCAT	711	Human respiratory syncytial virus
PMRSV_00007	TTTATGATGCAGCCAAAGCA	712	Human respiratory syncytial virus
PMRSV_00008	TCCATGAAATTCAAGGTGCAA	713	Human respiratory syncytial virus

id	Sequence (5' - 3')	SEQ ID NO:	species
PMRSV_00009	AAAAACACCCAGCCAAAACGA	714	Human respiratory syncytial virus
PMRSV_00010	CTGTGGGTGTTGTGTGGAG	715	Human respiratory syncytial virus
PMRSV_00011	CCAAAGCATATGCAGAGCAA	716	Human respiratory syncytial virus
PMRSV_00012	TCCATGAAATTCAAGTGCAA	717	Human respiratory syncytial virus
PMPI_00001	GCATGGAAACTAGCAGCACA	718	Parainfluenza
PMPI_00002	GGTGTGTTGGTCTTCGAGGT	719	Parainfluenza
PMPI_00003	GGCTCCATAGTATCATCGACAAC	720	Parainfluenza
PMPI_00004	CCTAGAGGCCCTGTGTATACCTT	721	Parainfluenza
PMPI_00005	ACACAACAAACAATGCAAACAAAC	722	Parainfluenza
PMPI_00006	TTAACATGCGCTTAGCAAATACA	723	Parainfluenza
PMPI_00007	TTAGCTCACTCATTGGACACAGA	724	Parainfluenza
PMPI_00008	GTCTCTCGTTTGACAATGAACC	725	Parainfluenza
PMPI_00009	TCTCACTACAAACGGTGTCAATG	726	Parainfluenza
PMPI_00010	TCTAGATCCGCATTCTCTCTTTG	727	Parainfluenza
PMPI_00011	ACAGATGGGTTCATTGTCAAAAC	728	Parainfluenza
PMPI_00012	GCTTTGACCAACACTATCCAAAC	729	Parainfluenza
PMPI_00013	GCTGAACACCCAGATTACAAAG	730	Parainfluenza
PMPI_00014	ACAGCTCTCCATTTCATGGTTTA	731	Parainfluenza
PMPI_00015	ATATGCATTGTCAATGGAGGAG	732	Parainfluenza
PMPI_00016	CATTGGTGTGTAAAATGCAAGA	733	Parainfluenza
PMPI_00017	CACAGAACACCCAGAACACAAGA	734	Parainfluenza
PMPI_00018	TTGGGACTGTTAACCAATACACC	735	Parainfluenza
PMME_00001	CATCCCAAAATTGCCAGAT	736	Human metapneumovirus

<u>id</u>	<u>Sequence (5' - 3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PMME_00002	TTTGGGCTTGCTTAAATG	737	Human metapneumovirus
PMME_00003	ACACCCTCATCATTGCAACA	738	Human metapneumovirus
PMME_00004	GCCCTTCTGACTGTGGTCTC	739	Human metapneumovirus
PMME_00005	CGACACAGCAGCAGGAATT	740	Human metapneumovirus
PMME_00006	TCAAAGCTGCTTGACACTGG	741	Human metapneumovirus

Please replace Table 20, beginning on page 61 and bridging to page 66, with a new Table 20 as follows:

Table 20. Exemplary primers for non-SARS-CoV infectious organism damaging the subject's immune system

<u>id</u>	<u>sequence (5' - 3')</u>	<u>SEQ. ID NO:</u>	<u>species</u>
PMTTV_00001	TGGGGCCAGACTTCGCCATA	742	TTV
PMTTV_00002	AGCTTCCGCCGAGGATGACC	743	TTV
PMTTV_00003	CTTGGGGGCTCAACGCCCTTC	744	TTV
PMTTV_00004	GCGAAGTCTGGCCCCACTCA	745	TTV
PMTTV_00005	CCACAGGCCAACCGAATGCT	746	TTV
PMTTV_00006	AGCCCGAATTGCCCTTGAC	747	TTV
PMTTV_00007	AGCGAATCCTGGAGTCAAACTCAG	748	TTV
PMTTV_00008	GGCCTCGTACTCCTCTTCAGTCA	749	TTV
PMTTV_00009	GCCCCTTGCATACCACTCAGACAT	750	TTV
PMTTV_00010	TGGAATGTGAGTTCCGGTGAGTTGT	751	TTV
PMTTV_00011	TGTCAGTAAACAGGGGTCGCCATAGA	752	TTV
PMTTV_00012	TGTGACGTATGGACGACCTTGACC	753	TTV
PMV_11047	CACAGACAGAGGAGAAGGCAAC	754	TTV
PMV_11048	AATAGGCACATTACTACTACCTCCTG	755	TTV

id	sequence(5' - 3')	SEQ ID NO:	species
PMTP_00001	GCGGTCGGTAGGAGGATAAAGGAAA	756	TP
PMTP_00002	CCGGGGATTTGTCTACAGGGTTCT	757	TP
PMTP_00003	CAGACGCTCATCCAACTCCTGAGAA	758	TP
PMTP_00004	CCGTTGTACCGTCTTTGGACGTT	759	TP
PMTP_00005	CACGCTCTACCTCATTGAGAGCAA	760	TP
PMTP_00006	GTTGTGTTGCAACGAAACACGCTACA	761	TP
PMTP_00007	AGCGGTCGGTAGGAGGATAAAGGAA	762	TP
PMTP_00008	ACCGGGGATTTGTCTACAGGGTTTC	763	TP
PMV_11025	AACACGATCCGCTACGACTACTAC	764	TP
PMV_11026	CCCTATAACCGTTCGCAATCAAAG	765	TP
PMHIV1_00001	ATGGGCGCAGCCTCAATGAC	766	HIV1
PMHIV1_00002	CCCCAAATCCCCAGGAGCTG	767	HIV1
PMHIV1_00003	GGGACAGCTACAACCATCCCTTCAG	768	HIV1
PMHIV1_00004	GACCTGATTGCTGTGTCCTGTCA	769	HIV1
PMHIV1_00005	GGGATGGAAAGGATCACCAAGCAATA	770	HIV1
PMHIV1_00006	GTCTGGTGTGGTAAGCCCCACCTC	771	HIV1
PMHIV1_00007	AAGGATCAACAGCTCCTGGGGATT	772	HIV1
PMHIV1_00008	TTCTTGCTGGTTTGCAGATTCTCA	773	HIV1
PMV_11055	TAATCCACCTATCCCAGTAGGAGAAAT	774	HIV1
PMV_11056	GGTCCTTGTCTTATGTCCAGAACG	775	HIV1
PMV_11057	TGGGAAGTTCAATTAGGAATACAC	776	HIV1
PMV_11058	TCCTACATACAAATCATCCATGTATTG	777	HIV1
PMHGV_00001	GCCGGCGATGACTGCTTGAT	778	HGV
PMHGV_00002	TCCGGAAGTCCGTGGTCAGG	779	HGV
PMHGV_00003	ACGGTGGGAGTCGCCTGAC	780	HGV
PMHGV_00004	GGCCACGCAAACCAACAAGG	781	HGV

id	sequence(5'- 3')	SEQ ID NO:	species
PMHGV_00005	CGGCCAAAAGGTGGTGGATG	782	HGV
PMHGV_00006	CGGGCTCGTTAACGACGA	783	HGV
PMHGV_00007	GCCACGGGAAAATCAGTGG	784	HGV
PMHGV_00008	TGTCGCGATCCGATGATCCA	785	HGV
PMHGV_00009	CGCGTGTGAGCTAAAGTGGGAAAGT	786	HGV
PMHGV_00010	ATCGTCACCAACAGGAAGACCATGA	787	HGV
PMHGV_00011	TCGCTCTCGGTTGGTTTGATTCT	788	HGV
PMHGV_00012	CATCCACCTTAGGCTCCCTGTTGAC	789	HGV
PMV_11045	GGGTTGGTAGGTCGAAATCCC	790	HGV
PMV_11046	GTACGTGGCGTCGTTGC	791	HGV
PMV_11001	CCTTCCACCATCCAGCAGT	792	HEV
PMV_11002	CGAGCTTACCCACCTTCAGC	793	HEV
PMHEV_00001	CTGGCGGTGGCTCTGTCT	794	HEV
PMHEV_00002	ACCGAGGCGGGAGCAAGTCT	795	HEV
PMHEV_00003	ACGGGCGGATCGATTGTGAG	796	HEV
PMHEV_00004	GGCAGCGACATAGCGCACCT	797	HEV
PMHEV_00005	AGCTCACCAACCACGGCTGCT	798	HEV
PMHEV_00006	CTGAGACGACGGGGCGAGAG	799	HEV
PMHEV_00007	ATCGCGCCCTTTCTGTCC	800	HEV
PMHEV_00008	GGGGCGACCATCAAGTGTG	801	HEV
PMHDV_00001	GACGGGCGGTGTTCTTCT	802	HDV
PMHDV_00002	GACTCCGGGCCTGGGAAGAG	803	HDV
PMHDV_00003	ACTCCGGCGAAAGGTGAG	804	HDV
PMHDV_00004	GGCGGAACACCCACCGACTA	805	HDV
PMHDV_00005	CCATGACTCTGGAGACATCCTGGAA	806	HDV
PMHDV_00006	CGTCAGAGCTCTGTTCGCTGAAG	807	HDV

<u>Id</u>	<u>Sequence (5' - 3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PMHDV_00007	CCTTCTCTCGTCTTCCTCGGTCAAC	<u>808</u>	HDV
PMHDV_00008	CCGAACGGACCAGATGGAGATAGAC	<u>809</u>	HDV
PMHDV_00009	GCTCCCGAGAGGGATAAAACGGTAA	<u>810</u>	HDV
PMHDV_00010	GAGTGCTCTCCAAACTTGGCAGTTG	<u>811</u>	HDV
PMHDV_00011	TCTCGTCTCCTCGGTCAACCTCTT	<u>812</u>	HDV
PMHDV_00012	CCGAACGGACCAGATGGAGATAGAC	<u>813</u>	HDV
PMV_11041	AACATTCCGAAGGGGACCGT	<u>814</u>	HDV
PMV_11042	GGCATCCGAAGGAGGACG	<u>815</u>	HDV
PMHCV_00001	GGCGCTGGAAAGAGGGTCTACTACC	<u>816</u>	HCV
PMHCV_00002	TGTTCAAGCTGATCCCTGGCTATGA	<u>817</u>	HCV
PMHCV_00003	ACATCTGGACTGGATATGCGAGGT	<u>818</u>	HCV
PMHCV_00004	ATCCTCATCGTCCCGTTTGACAT	<u>819</u>	HCV
PMHCV_00005	TGTGCCAGGACCATCTTGAATTGG	<u>820</u>	HCV
PMHCV_00006	AGGCGGATCAAACACTTCCACATCT	<u>821</u>	HCV
PMHCV_00007	GGGGTGCAAATGATACGGATGTCTT	<u>822</u>	HCV
PMHCV_00008	AGAGTATGTGGCTTCCGGATGCTTG	<u>823</u>	HCV
PMHCV_00009	ACACGCCGTGGGCCTATTCA	<u>824</u>	HCV
PMHCV_00010	GCCGGGACCTTGGTGCTCTT	<u>825</u>	HCV
PMHCV_00011	CACGCCGTGGGCCTATTCA	<u>826</u>	HCV
PMHCV_00012	GCCGGGACCTTGGTGCTCTT	<u>827</u>	HCV
PMV_11039	CTCGCAAGCACCCATCAGGCAGT	<u>828</u>	HCV
PMV_11040	GCAGAAAGCGTCTAGCCATGGCGT	<u>829</u>	HCV
PMHCMV_00001	GCGCCTGCTGCTCGAAATGT	<u>830</u>	HCMV
PMHCMV_00002	GTCGCGGCTGTTGCGGTAGT	<u>831</u>	HCMV
PMHCMV_00003	CCCCACGTCCATCTGCGTCT	<u>832</u>	HCMV
PMHCMV_00004	GCCCCCAGCAGTCTCACCAAG	<u>833</u>	HCMV

<u>Id</u>	<u>Sequence (5' - 3')</u>	<u>SEQ ID NO:</u>	<u>species</u>
PMHCMV_00005	GCTCACGCACCCCTGGAGGAC	834	HCMV
PMHCMV_00006	AGTTCCAGCCCACGCACCAAG	835	HCMV
PMHCMV_00007	GTGCAGTTAGGTGGCAGTCATGC	836	HCMV
PMHCMV_00008	GGAAAGGGGAGGGTAGAAACGTGAG	837	HCMV
PMHCMV_00009	TGTGATTGCGTGTGCAGTTAGGTG	838	HCMV
PMHCMV_00010	GGGGAGGGTAGAAACGTGAGTCTCC	839	HCMV
PMV_11051	ATTCCAAGCGGCCTCTGATAA	840	HCMV
PMV_11052	TCTTCCTCTGGGGCAACTTCC	841	HCMV
PMHBV_00001	TCGCAGTCCCCAACCTCCAA	842	HBV
PMHBV_00002	CAGGGTCCCGTGCTGGTTGT	843	HBV
PMHBV_00003	GCAGCCGGTCTGGAGCAAAA	844	HBV
PMHBV_00004	GCAGACGGAGAAGGGGACGA	845	HBV
PMHBV_00005	CGCCTCATTTGCGGGTCAC	846	HBV
PMHBV_00006	TGGTTGGCTTGTGGCAGTG	847	HBV
PMHBV_00007	ATCAAGGTATGTTGCCGTTGTCC	848	HBV
PMHBV_00008	AGGCCCACTCCCATAGGTATTTGC	849	HBV
PMHBV_00009	CCTAGGACCCCTGCTCGTGTACAG	850	HBV
PMHBV_00010	GCGATAACCAGGACAAATTGGAGGA	851	HBV
PMHBV_00011	CTGCGCACCATATTATGCAACTTT	852	HBV
PMHBV_00012	AGTAGATCCGGACGGAAGGAAAGA	853	HBV
PMV_11037	GTTCAAGCCTCCAAGCTGTG	854	HBV
PMV_11038	TCAGAAGGCCAAAAAGAGAGTAAC	855	HBV
PMHAV_00001	GATGTTGGGACGTACCTT	856	HAV
PMHAV_00002	CTGGATGAGAGCCAGTCCTC	857	HAV
PMHAV_00003	ATTGCATTGGCAACCAAAAT	858	HAV
PMHAV_00004	ATCTCATTGGGCATCCTGAC	859	HAV

id	sequence (5' - 3')	SEQ. ID NO.	species
PMHAV_00005	GACTGGAGGTTGGGAAACAA	860	HAV
PMHAV_00006	AGCAGCCAGAGAGAACCAA	861	HAV
PMHAV_00007	TAAGCATTTCGGCAAAG	862	HAV
PMHAV_00008	AGGCATTGACCCATCTC	863	HAV
PMHAV_00009	CCAACCAAATATCATTGAGTAGAC	864	HAV
PMHAV_00010	GACTTCGTGTACCTATTCACTCGAT	865	HAV
PMHAV_00011	GGGTTTCCTTATGTTCAAGAAAAAT	866	HAV
PMHAV_00012	CCAAAACCTTCTCTAATGGTCTCAA	867	HAV
PMV_11035	TTTGCTCCTCTTACCATGCTATG	868	HAV
PMV_11036	GGAAATGTCTCAGGTACTTCTTTG	869	HAV
PMEBV_00001	AACCCAATAGCATGACAGCCAATCC	870	EBV
PMEBV_00002	TCAGCCCCAGAGACACGGTATATGA	871	EBV
PMEBV_00003	TGAACCTGGGACCTATTGATGCAGA	872	EBV
PMEBV_00004	CAGGGGAATCTCTGCCAACTTGAG	873	EBV
PMEBV_00005	TGCACAGTGACAGTGGGAGAAACAC	874	EBV
PMEBV_00006	AAGAATGAAAGGGTGGCAGTGTG	875	EBV
PMEBV_00007	GTGCACAGTGACAGTGGGAGAAACA	876	EBV
PMEBV_00008	AAGAATGAAAGGGTGGCAGTGTG	877	EBV
PMV_11053	CCACGCGCGATAATG	878	EBV
PMV_11054	TTCACTTCGGTCTCCCTAG	879	EBV
PMB19_00001	TGGGCCGCCAAGTACAGGAA	880	B19
PMB19_00002	GGGTTGCCGCCCTAAATGG	881	B19
PMB19_00003	CCCTATTAGTGGGGCAGCATGTGTT	882	B19
PMB19_00004	CCACCAAGCTTTCCCTGCTACATC	883	B19
PMB19_00005	CAGTGTACAGCCATACCACTG	884	B19
PMB19_00006	TGCTGGGTTCCCTTATTGGGAAAT	885	B19

id	sequence(5'- 3')	SEQ ID NO:	species
PMB19_00007	CCCATTGCATTAATGTAGGGGCTTG	<u>886</u>	B19
PMB19_00008	ATCACTTCCCACCATTGCCACTT	<u>887</u>	B19
PMV_11049	CCTTCCACCATCCAGCACT	<u>888</u>	B19
PMV_11050	CGAGCTTACCCACCTTCAGC	<u>889</u>	B19

Please replace Table 21, beginning on page 66 and bridging to page 68, with a new Table 21 as follows:

Table 21. Exemplary primers for non-SARS-CoV coronaviridae virus

seqid	sequence(5'-3')	SEQ ID NO:
PMIBV_00001	GGAACAGGACCTGCCGCTGA	<u>890</u>
PMIBV_00002	ATCAGGTCCGCCATCCGAGA	<u>891</u>
PMIBV_00003	AAAGGTGGAAGAAAACCAGTCCCAGA	<u>892</u>
PMIBV_00004	GCCATCCGAGAATCGTAGTGGTATT	<u>893</u>
PMMHV_00001	CAGCGCCAGCCTGCCTCTAC	<u>894</u>
PMMHV_00002	TGCTGCACTGGGCACTGCTT	<u>895</u>
PMMHV_00003	GGAAATTACCGACTGCCCTCAAACA	<u>896</u>
PMMHV_00004	TGATTATTGGTCCACGCTCGTTT	<u>897</u>
PMEQ_00001	TCCCGCGCATCCAGTAGAGC	<u>898</u>
PMEQ_00002	CTGCGGCTTGTGGCATCCT	<u>899</u>
PMEQ_00003	TTTGCTGAAGGACAAGGTGTGCCTA	<u>900</u>
PMEQ_00004	CCAGAAGACTCCGTCATGTTGGTG	<u>901</u>
PMCA_00001	AAAAACGTGGTCGTTCCAATTCTCG	<u>902</u>
PMCA_00002	CCATGCGATAGCGGCTTGTCTATT	<u>903</u>
PMCA_00003	TGGGAACGGTGCCAAGCATT	<u>904</u>
PMCA_00004	GCCACCTCTGATGGACGAGCA	<u>905</u>
PMFE_00001	CGCGTCAACTGGGGAGATGAA	<u>906</u>
PMFE_00002	GCGCGCCTGTCTGTTCCAAT	<u>907</u>
PMFE_00003	GAGTCTTCTGGGTTGCAAAGGATGG	<u>908</u>

seqid	sequence (5'-3')	SEQ ID NO:
PMFE 00004	CCCCCTGGATTGAGACCTGTTCTTG	<u>909</u>
PMPEDV 00001	GCAGCATTGCTCTTGGTGGTAATG	<u>910</u>
PMPEDV 00002	TGCTGAATGGTTCACGCTTGTCT	<u>911</u>
PMPEDV 00003	CCGAAACGGGTGCCATTAT	<u>912</u>
PMPEDV 00004	TCGCCGTGAGGTCCCTGTTCC	<u>913</u>
PMPTGV 00001	TCGCTCCAATTCCCCTGGTC	<u>914</u>
PMPTGV 00002	ACGTTGCCCTTCACCATGC	<u>915</u>
PMPTGV 00003	CAAGCATTACCCACAATTGGCTGAA	<u>916</u>
PMPTGV 00004	TTCTTTGCCACTTCTGATGGACGA	<u>917</u>
PMBOV 00001	TTCCTTTAAAACAGCCGATGGCAAC	<u>918</u>
PMBOV 00002	TCGGAATAGCCTCATCGCTACTTGG	<u>919</u>
PMBOV 00003	TTCCGCCTGGCACGGTACTC	<u>920</u>
PMBOV 00004	TGGCTTAGCGGCATCCTTGC	<u>921</u>
PMFIPV 00001	CACCATGGCCTCAGCCTTGA	<u>922</u>
PMFIPV 00002	GTGCCGCCAACCTGCCAGTA	<u>923</u>
PMFIPV 00003	GGTCTTGGCACTGTGGATGATGATT	<u>924</u>
PMFIPV 00004	GAAAAAAGGGACAGCTACAGCGGATG	<u>925</u>
PMR 00001	CCCAATCAGAATTGGAGGCTCTG	<u>926</u>
PMR 00002	AGCGAATTGCACCTGAATACTGCAA	<u>927</u>
PMR 00003	TGACCAAACCGAGCGTGCAG	<u>928</u>
PMR 00004	CAGTGGCGGGATTCCATTG	<u>929</u>
PMPEV 00001	AGCGTCAACTGCTGCCACGA	<u>930</u>
PMPEV 00002	AGTACCGTGCCAGGCGGAAA	<u>931</u>
PMPEV 00003	AAGGTGTGCCTATTGCACCAGGAGT	<u>932</u>
PMPEV 00004	ACTAGCGACCCAGAAGACTCCGTCA	<u>933</u>
PMPV 00001	AGAAGACCACTGGGCTGACCAAAC	<u>934</u>
PMPV 00002	TTGGCAATAGGCACTCCTGTCCCT	<u>935</u>
PMPV 00003	GCGCCAGCCTGCCTCTATTG	<u>936</u>
PMPV 00004	TGGGGCCCCCTTTCCAAAAA	<u>937</u>

seqid	sequence (5' -3')	SEQ ID NO:
PMTK 00001	ATGGCTCACCGCCGGTATTG	<u>938</u>
PMTK 00002	TGGGCGTCACCTCTGCTTCCA	<u>939</u>
PMTK 00003	GCTAAGGCTGATGAAATGGCTCACC	<u>940</u>
PMTK 00004	TCCAAAAAGACAAGCATGGCTGCTA	<u>941</u>
PMSDAV 00001	TCTATGTTGAAGGCTCGGAAGGTC	<u>942</u>
PMSDAV 00002	TACTTGCTTAGGCTGTCCGGCATCT	<u>943</u>
PMSDAV 00003	AGCAGTGCCAGTGCAGCAG	<u>944</u>
PMSDAV 00004	TGGGTTCATCAACGCCACCA	<u>945</u>